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CM protein - protein search, using sw model

Run on: December 6, 2004, 15:11:52 ; Search time 145 Seconds
 Perfect score: 404 (without alignments)
 Sequence: 1 MAAGTAGAVVLVLSLWGAV.....RAELNQSEEPEAGESSTGGP 404

Title: US-10-069-598-1

Scoring table: Gapext 60.0 , Gapext 60.0

Searched: 1582122 seqs, 356623098 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgns_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 3: /cgns_6/ptodata/1/pubpaa/US05_PUBCOMB.pep:*
- 4: /cgns_6/ptodata/1/pubpaa/US04_PUBCOMB.pep:*
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- 9: /cgns_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgns_6/ptodata/1/pubpaa/US98_PUBCOMB.pep:*
- 11: /cgns_6/ptodata/1/pubpaa/OS09_PUBCOMB.pep:*
- 12: /cgns_6/ptodata/1/pubpaa/OS09_NEW_PUB.pep:*
- 13: /cgns_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgns_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
- 15: /cgns_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 16: /cgns_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgns_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 18: /cgns_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgns_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgns_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	404	100.0	404	Sequence 96, Appl
2	338	83.7	339	Sequence 3, Appl
3	337	83.4	390	Sequence 98, Appl
4	337	83.4	390	Sequence 100, Appl
5	332	82.2	332	Sequence 2, Appl
6	332	82.2	332	Sequence 1, Appl
7	216	53.5	405	Sequence 4, Appl
8	216	53.5	405	Sequence 4, Appl
9	207	51.2	342	Sequence 641, Appl
10	112	27.7	112	Sequence 1, Appl
11	30	7.4	30	Sequence 3, Appl
12	30	7.4	30	Sequence 7, Appl
13	30	7.4	30	Sequence 7, Appl

ALIGNMENTS

RESULT 1	US-10-09-290-96	Sequence 96, Application US/10309290
		GENERAL INFORMATION:
		APPLICANT: Alsobrook II, John P.
		APPLICANT: Anderson, David W.
		APPLICANT: Baldog, Perenc L.
		APPLICANT: Burgess, Catherine E.
		APPLICANT: Chiklaturu, Rajeev A.
		APPLICANT: Edinger, Shlomit R.
		APPLICANT: Gerlach, Valerie L.
		APPLICANT: Gorman, Linda
		APPLICANT: Gould-Bothberg, Bonnie E.
		APPLICANT: Guo, Xiaojia
		APPLICANT: Jeffers, Michael E.
		APPLICANT: Ji, Weizhen
		APPLICANT: Li, Li
		APPLICANT: Malyankar, Uriel M.
		APPLICANT: Murphy, Ryan
		APPLICANT: Paturajan, Meera
		APPLICANT: Peyman, John A.
		APPLICANT: Rastelli, Luca
		APPLICANT: Rieger, Daniel K.
		APPLICANT: Shenvoy, Suresh G.
		APPLICANT: Smithson, Glennanda
		APPLICANT: Starling, Gary
		APPLICANT: Taupier, Raymond J.
		APPLICANT: Voss, Edward Z.
		APPLICANT: Zhong, Haihong
		TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
		FILE REFERENCE: 21402-502A
		CURRENT APPLICATION NUMBER: US/10/309-290
		CURRENT FILING DATE: 2002-12-02

PRIOR APPLICATION NUMBER: 60/335,600
 PRIOR FILING DATE: 2001-12-05
 PRIOR APPLICATION NUMBER: 60/338,285
 PRIOR FILING DATE: 2001-12-07
 PRIOR APPLICATION NUMBER: 60/341,346
 PRIOR FILING DATE: 2001-12-12
 PRIOR APPLICATION NUMBER: 60/341,477
 PRIOR FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: 60/341,540
 PRIOR FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: 60/342,592
 PRIOR FILING DATE: 2001-12-20
 PRIOR APPLICATION NUMBER: 60/344,297
 PRIOR FILING DATE: 2001-12-27
 PRIOR APPLICATION NUMBER: 60/344,903
 PRIOR FILING DATE: 2001-12-31
 PRIOR APPLICATION NUMBER: 60/373,288
 PRIOR FILING DATE: 2002-04-17
 PRIOR APPLICATION NUMBER: 60/380,981
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 274
 SEQ ID NO: 96
 LENGTH: 404
 SOFTWARE: CuraseqList version 0.1
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-309-90-96

Query Match 100.0%; Score 404; DB 15; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGTAGAWLVLISLNGAVGAQNTIARIGPVLWKCGAPKKPPORLEWKLNTRTEA 60
 Db 1 MAAGTAGAWLVLISLNGAVGAQNTIARIGPVLWKCGAPKKPPORLEWKLNTRTEA 60

Qy 61 WKVLSPOGGGPWDSVARVLPNSSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVRVYQI 120
 Db 61 WKVLSPOGGGPWDSVARVLPNSSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVRVYQI 120

Qy 61 PGKPEIVDASSELTAGYPNKGTVSEGSSYPAQTLSWHLDGKPLVNEKGYSVKETQRHH 180
 Db 61 PGKPEIVDASSELTAGYPNKGTVSEGSSYPAQTLSWHLDGKPLVNEKGYSVKETQRHH 180

Qy 121 PGKPEIVDASSELTAGYNKGTVSEGSSYPAQTLSWHLDGKPLVNEKGYSVKETQRHH 180
 Db 121 PGKPEIVDASSELTAGYNKGTVSEGSSYPAQTLSWHLDGKPLVNEKGYSVKETQRHH 180

Qy 181 PETGLFTLQSELMVTPARGGIDPRTFSCSFEPGLPHRAUTAPICPRVWFPVPBEVOL 240
 Db 181 PETGLFTLQSELMVTPARGGDPRTFSCSFEPGLPHRAUTAPICPRVWFPVPBEVQL 240

Qy 241 VVEPEGGAVAPGTIVTLCVPAQPSQIHNMKDGVPPLPBPSPVLTPEIGPQDQGTS 300
 Db 241 VVEPEGGAVAPGTIVTLCVPAQPSQIHNMKDGVPPLPBPSPVLTPEIGPQDQGTS 300

Qy 301 CVATHSHGPQESRAVISIILEPGEDEPTASSVGSSL 338
 Db 301 CVATHSHGPQESRAVISIILEPGEDEPTASSVGSSL 338

RESULT 3
 US-10-309-290-98
 Sequence 98, Application US/10309290
 Publication No. US20040023241A1
 GENERAL INFORMATION:
 APPLICANT: Alsobrook II, John P.
 APPLICANT: Anderson, David W.
 APPLICANT: Boldog, Ferenc L.
 APPLICANT: Burgess, Catherine E.
 APPLICANT: Chilliakuru, Rajeev A.
 APPLICANT: Edinger, Shlomit R.
 APPLICANT: Gerlach, Valerie L.
 APPLICANT: Gorman, Linda
 APPLICANT: Gould-Rothberg, Bonnie E.
 APPLICANT: Guo, Xiaojaia
 APPLICANT: Jeffers, Michael E.
 APPLICANT: Ji, Weizhen
 APPLICANT: Li, Li
 APPLICANT: Malayankar, Uriel M.
 APPLICANT: Miller, Charles E.
 APPLICANT: Murphrey, Ryan
 APPLICANT: Paturajan, Meera
 APPLICANT: Peyman, John A.
 APPLICANT: Rastelli, Luca
 APPLICANT: Rieger, Daniel K.
 APPLICANT: Shenoy, Suresh G.
 APPLICANT: Smithson, Glennanda
 APPLICANT: Starling, Gary
 APPLICANT: Taupier, Raymond J.
 APPLICANT: Voss, Edward Z.
 APPLICANT: Zhang, Haibong
 APPLICANT: Zhong, Mei

RESULT 2
 US-10-091-019-3
 Sequence 3, Application US/10091019
 Publication No. US20030166063A1
 GENERAL INFORMATION:
 APPLICANT: Harris, Robert B.
 APPLICANT: Shen, Jane M.
 APPLICANT: Shabazz, Manohair M.
 TITLE OF INVENTION: High Level Insect Expression of RAGE Proteins
 FILE REFERENCE: 41305-27055
 CURRENT APPLICATION NUMBER: US/10/091,019

; CURRENT FILING DATE: 2002-03-05
 ; PRIOR APPLICATION NUMBER: US 60/273,418
 ; PRIOR FILING DATE: 2001-03-05
 ; NUMBER OF SEQ ID NOS: 10
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 3
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-091-019-3

Query Match 83.7%; Score 338; DB 14;
 Best Local Similarity 100.0%; Pred. No. 9.4e-290;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGTAGAWLVLISLNGAVGAQNTIARIGPVLWKCGAPKKPPORLEWKLNTRTEA 60
 Db 1 MAAGTAGAWLVLISLNGAVGAQNTIARIGPVLWKCGAPKKPPORLEWKLNTRTEA 60

Qy 61 WKVLSPOGGGPWDSVARVLPNSSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVRVYQI 120
 Db 61 WKVLSPOGGGPWDSVARVLPNSSLFLPAVGIDQEGIFRCQAMNRNGKETKSNYRVRVYQI 120

Qy 61 PGKPEIVDASSELTAGYPNKGTVSEGSSYPAQTLSWHLDGKPLVNEKGYSVKETQRHH 180
 Db 61 PGKPEIVDASSELTAGYPNKGTVSEGSSYPAQTLSWHLDGKPLVNEKGYSVKETQRHH 180

Qy 121 PGKPEIVDASSELTAGYNKGTVSEGSSYPAQTLSWHLDGKPLVNEKGYSVKETQRHH 180
 Db 121 PGKPEIVDASSELTAGYNKGTVSEGSSYPAQTLSWHLDGKPLVNEKGYSVKETQRHH 180

Qy 181 PETGLFTLQSELMVTPARGGIDPRTFSCSFEPGLPHRAUTAPICPRVWFPVPBEVOL 240
 Db 181 PETGLFTLQSELMVTPARGGDPRTFSCSFEPGLPHRAUTAPICPRVWFPVPBEVQL 240

Qy 241 VVEPEGGAVAPGTIVTLCVPAQPSQIHNMKDGVPPLPBPSPVLTPEIGPQDQGTS 300
 Db 241 VVEPEGGAVAPGTIVTLCVPAQPSQIHNMKDGVPPLPBPSPVLTPEIGPQDQGTS 300

Qy 301 CVATHSHGPQESRAVISIILEPGEDEPTASSVGSSL 338
 Db 301 CVATHSHGPQESRAVISIILEPGEDEPTASSVGSSL 338

FILE REFERENCE: 21402-502A
; CURRENT APPLICATION NUMBER: US/10/309,290
; CURRENT FILING DATE: 2002-12-02
; PRIOR APPLICATION NUMBER: 60/336,600
; PRIOR FILING DATE: 2001-12-05
; PRIOR APPLICATION NUMBER: 60/338,285
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/341,346
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/341,477
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/341,540
; PRIOR FILING DATE: 2001-12-17
; PRIOR APPLICATION NUMBER: 60/342,592
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/344,297
; PRIOR FILING DATE: 2001-12-27
; PRIOR APPLICATION NUMBER: 60/344,903
; PRIOR FILING DATE: 2001-12-31
; PRIOR APPLICATION NUMBER: 60/373,288
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 60/380,981
; PRIOR FILING DATE: 2002-05-15
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO: 98
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-309-290-98

Query Match 83.4% Score 337; DR 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.1e-289; Indels 0; Gaps 0;
Matches 337; Conservative 0; Mismatches 0;

Qy 68 GGCPWDSTARYLVLNGSLFLPAVGQIODEGIFRCAMNTRGKETKSNSYRVYQIPGKEIV 127
Db 54 GGCPWDSTARYLVLPGNSLFLPAVGQIODEGIFRCAMNTRGKETKSNSYRVYQIPGKEIV 113

Qy 128 DSASELTAGVPNPKVGTCVSEGSYPAGTSLWHDGKPLVNPNEKVSKEQTRRHPETGLFT 187
Db 114 DSASELTAGVPNPKVGTCVSEGSYPAGTSLWHDGKPLVNPNEKVSKEQTRRHPETGLFT 173

Qy 188 LOSBLMTPARGGDPRTFCSFSPLPQSPQTHMKDGYPLPLPPSPVILPLIGPODGTYSCVATHSS 307
Db 174 LQSBLLMTPARGGDPRTFCSFSPLPQSPQTHMKDGYPLPLPPSPVILPLIGPODGTYSCVATHSS 293

Qy 248 AVAPGGTVTTLTCVPAQSPQTHMKDGYPLPLPPSPVILPLIGPODGTYSCVATHSS 307
Db 234 AVAPGGTVTTLTCVPAQSPQTHMKDGYPLPLPPSPVILPLIGPODGTYSCVATHSS 293

Qy 308 HGQESRAVSISIEPGBEGPTAGSGSGLTIALALIGLGLTALLIGVILWORQ 367
Db 294 HGQESRAVSISIEPGBEGPTAGSGSGLTIALALIGLGLTALLIGVILWORQ 353

Qy 368 RRGERKAPENQEEERAAELNOSEEEPEAGESSTGGP 404
Db 354 RRGERKAPENQEEERAAELNOSEEEPEAGESSTGGP 390

RESULT 4
US-10-309-290-100
Sequence 100, Application US/10309290
Publication No. US20040023241A1
GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.

; APPLICANT: Gorman, Linda
; APPLICANT: Gould-Rothberg, Bonnie E.
; APPLICANT: Guo, Xiaojia
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Ji, Weizhen
; APPLICANT: Li, Li
; APPLICANT: Malyankar, Uriel M.
; APPLICANT: Miller, Charles E.
; APPLICANT: Murphy, Ryan
; APPLICANT: Patturajan, Meera
; APPLICANT: Peyman, John A.
; APPLICANT: Rastelli, Luca
; APPLICANT: Rieger, Daniel K.
; APPLICANT: Shenoy, Suresh G.
; APPLICANT: Smithson, Glennada
; APPLICANT: Starling, Gary
; APPLICANT: Taufer, Raymond J.
; APPLICANT: Voss, Edward Z.
; APPLICANT: Zhong, Hainong
; APPLICANT: Zhong, Mei

TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
FILE REFERENCE: 21402-502A
CURRENT APPLICATION NUMBER: US/10/309,290
PRIOR APPLICATION NUMBER: 60/336,600
PRIOR FILING DATE: 2001-12-05
PRIOR APPLICATION NUMBER: 60/338,285
PRIOR FILING DATE: 2001-12-07
PRIOR APPLICATION NUMBER: 60/341,346
PRIOR FILING DATE: 2001-12-12
PRIOR APPLICATION NUMBER: 60/341,477
PRIOR FILING DATE: 2001-12-17
PRIOR APPLICATION NUMBER: 60/342,592
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/344,297
PRIOR FILING DATE: 2001-12-27
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR FILING DATE: 2001-12-31
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: 60/344,903
PRIOR FILING DATE: 2002-05-15
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 274
SEQ ID NO: 100
TYPE: PRT
ORGANISM: Homo sapiens
US-10-309-290-100

Query Match 83.4% Score 337; DB 15; Length 390;
Best Local Similarity 100.0%; Pred. No. 8.1e-289; Indels 0; Gaps 0;
Matches 337; Conservative 0; Mismatches 0;

Qy 68 GGCPWDSTARYLVLNGSLFLPAVGQIODEGIFRCAMNTRGKETKSNSYRVYQIPGKEIV 127
Db 54 GGCPWDSTARYLVLPGNSLFLPAVGQIODEGIFRCAMNTRGKETKSNSYRVYQIPGKEIV 113

Qy 128 LOSBLMTPARGGDPRTFCSFSPLPQSPQTHMKDGYPLPLPPSPVILPLIGPODGTYSCVATHSS 307
Db 114 LQSBLLMTPARGGDPRTFCSFSPLPQSPQTHMKDGYPLPLPPSPVILPLIGPODGTYSCVATHSS 293

Qy 188 LOSBLMTPARGGDPRTFCSFSPLPQSPQTHMKDGYPLPLPPSPVILPLIGPODGTYSCVATHSS 307
Db 174 LQSBLLMTPARGGDPRTFCSFSPLPQSPQTHMKDGYPLPLPPSPVILPLIGPODGTYSCVATHSS 293

Qy 248 AVAPGGTVTTLTCVPAQSPQTHMKDGYPLPLPPSPVILPLIGPODGTYSCVATHSS 307
Db 234 AVAPGGTVTTLTCVPAQSPQTHMKDGYPLPLPPSPVILPLIGPODGTYSCVATHSS 293

Qy 308 HGQESRAVSISIEPGBEGPTAGSGSGLTIALALIGLGLTALLIGVILWORQ 367
Db 294 HGQESRAVSISIEPGBEGPTAGSGSGLTIALALIGLGLTALLIGVILWORQ 353

Qy 368 RRGERKAPENQEEERAAELNOSEEEPEAGESSTGGP 404
Db 354 RRGERKAPENQEEERAAELNOSEEEPEAGESSTGGP 390

RESULT 4
US-10-309-290-100
Sequence 100, Application US/10309290
Publication No. US20040023241A1
GENERAL INFORMATION:
; APPLICANT: Alsobrook II, John P.
; APPLICANT: Anderson, David W.
; APPLICANT: Boldog, Ferenc L.
; APPLICANT: Burgess, Catherine E.
; APPLICANT: Chilakuru, Rajeev A.
; APPLICANT: Edinger, Shlomit R.
; APPLICANT: Gerlach, Valerie L.

Qy 308 HGPQESPAVISIIEPQEPPAGTGSVGGSGLCTALALGILGGGLTAALLIGVIMQRQ 367
 Db 294 HGPQESPAVISIIEPQEPPAGTGSVGGSGLCTALALGILGGGLTAALLIGVIMQRQ 353

RESULT 5
 US-09-872-185B-2
 ; Sequence 2, Application US/09872185B
 ; Patent No. US2002012793A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Herold, Kevan
 ; APPLICANT: Yan, Shi Du
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Lamster, Ira
 ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
 ; FILE REFERENCE: 0575/64080
 ; CURRENT APPLICATION NUMBER: US/09/872,185B
 ; CURRENT FILING DATE: 2001-06-01
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 2
 ; LENGTH: 332
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-872-185B-2

Query Match 82.2%; Score 332; DB 9; Length 332;
 Best Local Similarity 100.0%; Pred. No. 1.8e-284;
 Matches 332; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AONITARIGEPLVLCKKGAKPKPQRLEWKINTGRTEAWKVLSPQQGGPMDSVARVLPNG 82
 Db 1 AONITARIGEPLVLCKKGAKPKPQRLEWKINTGRTEAWKVLSPQQGGPMDSVARVLPNG 60

Qy 83 SFLFLPAYIQDEGIFRQAMNRNGKETKSNYRVYQIPGKPEIVDASSELTAGVYNKG 142
 Db 61 SFLFLPAYIQDEGIFRQAMNRNGKETKSNYRVYQIPGKPEIVDASSELTAGVYNKG 120

Qy 143 TCVSEGSYPAGTSLWHLDGKLPVNEKGVSKEOTRRHPECLFTQSELMTPARGGDP 202
 Db 121 TCVSEGSYPAGTSLWHLDGKLPVNEKGVSKEOTRRHPECLFTQSELMTPARGGDP 180

Qy 203 RTPFSCSFSPGLPRLPRHRAARTAPIQPRWEPVPLEEVQLVVEPEGAVAPGGTVLTCEVP 262
 Db 181 RTPFSCSFSPGLPRLPRHRAARTAPIQPRWEPVPLEEVQLVVEPEGAVAPGGTVLTCEVP 240

Qy 263 AOPSPQIHWMKDGVPLPLPPSPVLLPEIGPODGTYSCVATHSHGPQESRAVSIIE 322
 Db 241 AOPSPQIHWMKDGVPLPLPPSPVLLPEIGPODGTYSCVATHSHGPQESRAVSIIE 300

Qy 323 PGEBEGPTAGSYYGSGGIGTLALALGILGGLGT 354
 Db 301 PGEBEGPTAGSYYGSGGIGTLALALGILGGLGT 332

RESULT 7
 US-08-755-235-4
 ; Sequence 4, Application US/08755235
 ; Publication No. US2003005943A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Wu, Jun
 ; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
 ; FILE REFERENCE: 0575/50159
 ; CURRENT APPLICATION NUMBER: US/08/755,235
 ; CURRENT FILING DATE: 1996-11-22
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 4
 ; LENGTH: 405
 ; TYPE: PRT
 ; ORGANISM: Human
 US-08-755-235-4

Query Match 53.5%; Score 216; DB 8; Length 405;
 Best Local Similarity 100.0%; Pred. No. 5.7e-182;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 AMNRNGKETKSNYRVYQIPGKPEIVDASSELTAGVYNKGTCSEGSYPAGTSLWHLD 160
 Db 101 AMNRNGKETKSNYRVYQIPGKPEIVDASSELTAGVYNKGTCSEGSYPAGTSLWHLD 160

Qy 161 GKPLVNEKGVSKEOTRRHPECLFTQSELMTPARGGDPRTCSFSGLPHRAL 220
 Db 161 GKPLVNEKGVSKEOTRRHPECLFTQSELMTPARGGDPRTCSFSGLPHRAL 220

Qy 221 RTPAPIQPRWEPVPLEEVQLVVEPEGAVAPGGTVLTCEVPQSPQIHWMKDGVPLPL 280
 Db 221 RTPAPIQPRWEPVPLEEVQLVVEPEGAVAPGGTVLTCEVPQSPQIHWMKDGVPLPL 280

Qy 281 PRSPVLLPEIGPODGTYSCVATHSHGPQESRAV 316
 Db 301 PRSPVLLPEIGPODGTYSCVATHSHGPQESRAV 316

RESULT 6
 US-09-851-071-1
 ; Sequence 1, Application US/09851071
 ; General Information:
 ; APPLICANT: Schmidt, Anne Marie
 ; APPLICANT: Stern, David
 ; TITLE OF INVENTION: A METHOD FOR INHIBITTING TUMOR INVASION OR SPREADING IN A SUBJECT
 ; FILE REFERENCE: 0575/55424-7.JPW.SHS/IMM
 ; CURRENT FILING DATE: 2001-05-08
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.1

Db	281	FPSPVLLPEIGPQDGTYSSCVATHSSHGPQESRAV	316	Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps
RESULT 8				
; Sequence 4, Application US/10850861				
; Publication No. US20041028855A1				
; GENERAL INFORMATION:				
; APPLICANT: Stern, David M.				
; APPLICANT: Schmidt, Ann Marie				
; APPLICANT: Wu, Jun				
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES				
; FILE REFERENCE: 0575/20159				
; CURRENT FILING DATE: 2004-05-20				
; PRIOR APPLICATION NUMBER: US/08/755,235				
; PRIOR FILING DATE: 1998-11-22				
; NUMBER OF SEQ ID NOS: 4				
; SOFTWARE: PatentIn version 3.1				
; SEQ ID NO 4				
; LENGTH: 405				
; TYPE: PRT				
; ORGANISM: Human				
US-10-850-861-4				
Query Match Score 53.5%; Score 216; DB 17; Length 405;				
Best Local Similarity 100.0%; Pred. No. 5.7e-182;				
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
;				
Qy	101	AMNRNGKETKSNYRVRVYQIPGKPEIVDSAELTAGENKVGETCSEGSSYPAGTLLSNHLD	160	;
Db	101	AMNRNGKETKSNYRVRVYQIPGKPEIVDSAELTAGENKVGETCSEGSSYPAGTLLSNHLD	160	;
Qy	161	GKPLVNEKGYSVKEOTRRHPETGLFTLQSELMVTARGGDPRPTESSESFGPLPRHAL	220	;
Db	161	GKPLVNEKGYSVKEOTRRHPETGLFTLQSELMVTARGGDPRPTESSESFGPLPRHAL	220	;
Qy	221	RTAPIOPRWRWEPVPLEVQLVYVEPEGGAVAPGTVLTCEVPAQSPQIHMMDGVPLPL	280	;
Db	221	RTAPIOPRWRWEPVPLEVQLVYVEPEGGAVAPGTVLTCEVPAQSPQIHMMDGVPLPL	280	;
Qy	281	FPSPVLLPEIGPQDGTYSSCVATHSSHGPQESRAV	316	;
Db	281	FPSPVLLPEIGPQDGTYSSCVATHSSHGPQESRAV	316	;
RESULT 9				
; Sequence 641, Application US/10408765A				
; Publication No. US2004101874A1				
; GENERAL INFORMATION:				
; APPLICANT: Ghosh, Soumitra S.				
; APPLICANT: Fahy, Eoin D.				
; APPLICANT: Zhang, Bing				
; APPLICANT: Gibson, Bradford W.				
; APPLICANT: Taylor, Steven W.				
; APPLICANT: Glenn, Gary M.				
; APPLICANT: Warnock, Dale E.				
; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME				
; FILE REFERENCE: 660088465				
; CURRENT FILING DATE: 2003-04-04				
; NUMBER OF SEQ ID NOS: 3077				
; SOFTWARE: FastSEQ for Windows Version 4.0				
; SEQ ID NO 641				
; LENGTH: 342				
; TYPE: PRT				
; ORGANISM: Homo sapiens				
US-10-408-765A-641				
Query Match Score 51.2%; Score 207; DB 16; Length 342;				
Best Local Similarity 100.0%; Pred. No. 4.4e-174;				

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/948,131
 FILING DATE: 09-OCT-1997
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: White, John P.
 REFERENCE/DOCKET NUMBER: 28, 678
 TELECOMMUNICATION INFORMATION:
 TELEFAX: 212-391-0526
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-948-131-1

Query Match 7.4%; Score 30; DB 8; Length 30;
 Best Local Similarity 100.0%; Pred. No. 9.9e-19;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AQNITARIGEPLVKCKGAPKKPPQRLEWK 52
 Db 1 AQNITARIGEPLVKCKGAPKKPPQRLEWK 30

RESULT 12
 US-09-872-185B-3
 Sequence 3, Application US/09872185B
 ; Patent No. US20020122799A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Herold, Kevan
 ; APPLICANT: Yan, Shi Du
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Lamster, Ira
 ; TITLE OF INVENTION: METHODS FOR TREATING INFLAMMATION
 ; FILE REFERENCE: 0575/64080
 ; CURRENT APPLICATION NUMBER: US/08/872,185B
 ; CURRENT FILING DATE: 2001-06-01
 ; NUMBER OF SEQ ID NOS: 16
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 3
 ; LENGTH: 30
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-872-185B-3

Query Match 7.4%; Score 30; DB 9; Length 30;
 Best Local Similarity 100.0%; Pred. No. 9.9e-19;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AQNITARIGEPLVKCKGAPKKPPQRLEWK 52
 Db 1 AQNITARIGEPLVKCKGAPKKPPQRLEWK 30

RESULT 13
 US-09-872-185B-7
 Sequence 7, Application US/09872185B
 ; Patent No. US20020122799A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Herold, Kevan
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Stern, David M.

Query Match 5.9%; Score 24; DB 8; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.9e-12;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 237 EVOLVVEPEGGAVAPGGTVTLTCB 260
Db 247 EVOLVVEPEGGAVAPGGTVTLTCB 270

Search completed: December 6, 2004, 15:21:52
Job time : 147 secs



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GenCore version 5.1.6

OM protein - protein search, using SW model

Run on: December 6, 2004, 15:08:41 ; Search time 39 Seconds
 (without alignment)
 686.986 Million cell updates/sec

Title: US-10-069-598-1

Perfect score: 404

Sequence: 1 MAAGTAGAWVLVLSLNGAV.....RAELNQSEEPEAGESSTGGP 404

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 478139 seqs, 66318000 residues

Word size : 0

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgns_6/ptodata/1/iaa/5A_COMB.pep:
 2: /cgns_6/ptodata/1/iaa/5B_COMB.pep:
 3: /cgns_6/ptodata/1/iaa/5A_COMB.pep:
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 5: /cgns_6/ptodata/1/iaa/PCTUS_COMB.pep:
 6: /cgns_6/ptodata/1/iaa/backtles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	340	84.2	340	2	US-08-633-148-2	Sequence 1, Appli
2	332	82.2	332	4	US-08-633-365-1	Sequence 1, Appli
3	318	78.7	318	2	US-08-633-148-4	Sequence 4, Appli
4	304	75.2	404	4	US-08-638-649-3	Sequence 3, Appli
5	216	53.5	405	4	US-08-755-235-4	Sequence 4, Appli
6	207	51.2	278	2	US-08-433-016-5	Sequence 5, Appli
7	207	51.2	278	2	US-08-684-594-5	Sequence 2, Appli
8	30	7.4	30	4	US-09-062-365-5	Sequence 5, Appli
9	30	7.4	30	4	US-08-948-131-1	Sequence 1, Appli
10	26	6.4	403	4	US-09-638-649-5	Sequence 4, Appli
11	24	5.9	278	2	US-08-755-235-2	Sequence 1, Appli
12	24	5.9	416	4	US-08-633-148-15	Sequence 2, Appli
13	22	5.4	22	4	US-09-062-365-2	Sequence 5, Appli
14	16	4.0	16	2	US-08-633-148-18	Sequence 18, Appli
15	15	3.7	15	2	US-08-633-148-12	Sequence 12, Appli
16	13	3.2	30	4	US-08-948-131-2	Sequence 2, Appli
17	11	2.7	11	2	US-08-633-148-9	Sequence 9, Appli
18	11	2.7	11	2	US-08-633-148-15	Sequence 15, Appli
19	11	2.7	30	4	US-08-948-131-3	Sequence 3, Appli
20	10	2.5	10	2	US-08-633-148-5	Sequence 5, Appli
21	10	2.5	10	2	US-08-633-148-7	Sequence 7, Appli
22	10	2.5	10	2	US-08-633-148-8	Sequence 8, Appli
23	10	2.5	10	2	US-08-633-148-11	Sequence 11, Appli
24	10	2.5	10	2	US-08-633-148-13	Sequence 13, Appli
25	10	2.5	10	2	US-08-633-148-16	Sequence 16, Appli
26	10	2.5	10	2	US-08-633-148-17	Sequence 17, Appli
27	10	2.5	10	4	US-09-062-365-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1
 US-08-633-148-2
 ; Sequence 2, Application US/08633148
 ; Patent No. 5866018
 ; GENERAL INFORMATION:
 ; APPLICANT: MORSER, MICHAEL J.
 ; NAGASHIMA, MARILKO
 ; HOLLANDER, DORIS A.
 ; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
 ; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
 ; CITY: SAN FRANCISCO
 ; STATE: CALIFORNIA
 ; COUNTRY: U.S.A.
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOSS/MS-DOS
 ; SOFTWARE: Parent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08-633, 148
 ; FILING DATE: 16-APR-1996
 ; CLASSIFICATION: 435.....
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURPHY ESQ., MATTHEW B.
 ; REGISTRATION NUMBER: 39,787
 ; REFERENCE DOCKET NUMBER: 014618-005600US
 ; TELECOMMUNICATION INFORMATION:
 ; TELEFAX: (415) 326-2400
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 340 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; Query Match 84.2%; Score 340; DB 2; Length 340;
 ; Best Local Similarity 100.0%; Pred. No. 2.4e-07;
 ; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MAGTAYGAWVLVLSLNGAVVGAQNITARIGEPLVLIKCGAPKKPPORLEWKNTGRTEA 60
 Db 1 MAGTAYGAWVLVLSLNGAVVGAQNITARIGEPLVLIKCGAPKKPPORLEWKNTGRTEA 60

QY 61 WKVLSPOGGPMDSVARVLPGNSLFLPAVGIODEGIFRCAMMRNGKETKSNYRVRVQI 120 ; Sequence 4, Application US/08633148
Db 61 WKVLSPOGGPMDSVARVLPGNSLFLPAVGIODEGIFRCAMMRNGKETKSNYRVRVQI 120 ; Patent No. 5664018
; GENERAL INFORMATION:
; APPLICANT: MORSER, MICHAEL J.
; APPLICANT: NAGASHIMA, MARIKO A.
; APPLICANT: HOLLANDER, DORIS A.
; TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
; TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND & TOWNSEND & CREW LLP
; STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,148
; FILING DATE: 16-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MURPHY ESO., MATTHEW B.
; REGISTRATION NUMBER: 39,787
; REFERENCE/DOCKET NUMBER: 014618-005600US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-4222
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 318 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; US-08-633-148-4

Query Match 82.2%; Score 332; DB 4; Length 332;
Best Local Similarity 100.0%; Pred. No. 6.2e-100; Indels 0; Gaps 0;
Matches 332; Conservative 0; Mismatches 0;

Qy 23 AQNITARIGEPLVKCKGAKPKPQLRKNTGRTEAWKVLSPQCGGPWDSSAVRLPNG 82
Db 1 AQNITARIGEPLVKCKGAKPKPQLRKNTGRTEAWKVLSPQCGGPWDSSAVRLPNG 60
Qy 83 SULFLPAYIQDEGIFRCAMMRNGKETKSNYRVRVQIPLGKPEIVDASELTAGVNKVG 142
Db 61 SULFLPAYIQDEGIFRCAMMRNGKETKSNYRVRVQIPLGKPEIVDASELTAGVNKVG 120
Qy 143 TCYSEGSTPAGTLIWHLDGKPLVNEPKVSVKEQTRHPETGLFTQSELMTPARGDGP 202
Db 121 TCYSEGSTPAGTLIWHLDGKPLVNEPKVSVKEQTRHPETGLFTQSELMTPARGDGP 180
Qy 203 RPTFSCSFSPGFLPRHRALRTAPIQPRWEPVPLREVQIPLPSSPVLLPGCTVLTCEVP 262
Db 181 RPTFSCSFSPGFLPRHRALRTAPIQPRWEPVPLREVQIPLPSSPVLLPGCTVLTCEVP 240
Qy 263 AQPSPQIWHMKDGYPLPLPPSPVLLPGCTVLTCEVP 322
Db 241 AQPSPQIWHMKDGYPLPLPPSPVLLPGCTVLTCEVP 300
Qy 323 PGEEGPTAGSVGSGLGT 340
Db 301 PGEEGPTAGSVGSGLGT 318

RESULT 4
US-09-638-649-3 ; Sequence 3, Application US/09638649

Patent No. 6563015
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Yan, Shi Du
; TITLE OF INVENTION: TRANSGENIC MICE OVER-EXPRESSING RECEPTOR FOR ADVANCED GLICATION ENDPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 0575/62175
; CURRENT APPLICATION NUMBER: US/09/638,649
; CURRENT FILING DATE: 2000-08-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Human
US-09-638-649-3

Query Match 75.2%; Score 304; DB 4; Length 404;
Best Local Similarity 100.0%; Pred. No. 7.3e-274; Indels 0; Gaps 0;
Matches 304; Conservative 0; Mismatches 0;

Qy 101 AMNRNGKETKSNYRVRVYQIPGKPEIVDSASELTAGVNKGTCVSEGSSYPA GTLSWHL D 160
Db 101 AMNRNGKETKSNYRVRVYQIPGKPEIVDSASELTAGVNKGTCVSEGSSYPA GTLSWHL D 160

Qy 161 GKLPVNKEKGVSYKEQTRHPETGLFTIQLSELMVTAPGGDPRPTFCSFSPLPRL 220
Db 161 GKLPVNKEKGVSYKEQTRHPETGLFTIQLSELMVTAPGGDPRPTFCSFSPLPRL 220

Qy 221 RTAPIQPRVWEPYPELVEQLVVEPEGGAVA PGGTVTLLCE VPQSPQIHMWDGVPL 280
Db 221 RTAPIQPRVWEPYPELVEQLVVEPEGGAVA PGGTVTLLCE VPQSPQIHMWDGVPL 280

Qy 281 PPSPVLILPEIGQDGTYSCVATHSHQPEAVSISIIEPGEEGPTAGSVGSSLGT 340
Db 281 PPSPVLILPEIGQDGTYSCVATHSHQPEAVSISIIEPGEEGPTAGSVGSSLGT 340

Qy . 341 LALALGIUGLGTAALLIGVLMQRQRGEREKAPENQEERERAELNQSEPEAGES 400
Db 341 LALALGIUGLGTAALLIGVLMQRQRGEREKAPENQEERERAELNQSEPEAGES 400

Qy . 401 TGGP 404
Db 401 TGSP 404

RESULT 5
US-08-755-235-4
; Sequence 4, Application US/08755235
; GENERAL INFORMATION:
; APPLICANT: Stern, David M.
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Wu, Jun
; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
; FILE REFERENCE: 0575/50159
; CURRENT APPLICATION NUMBER: US/08/755,235
; CURRENT FILING DATE: 1996-11-22
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 4
; LENGTH: 405
; TYPE: PRT
; ORGANISM: Human
US-08-755-235-4

Query Match 53.5%; Score 216; DB 4; Length 405;
Best Local Similarity 100.0%; Pred. No. 3.6e-192; Indels 0; Gaps 0;
Matches 216; Conservative 0; Mismatches 0;

Qy 101 AMNRNGKETKSNYRVRVYQIPGKPEIVDSASELTAGVNKGTCVSEGSSYPA GTLSWHL D 160
Db 72 AMNRNGKETKSNYRVRVYQIPGKPEIVDSASELTAGVNKGTCVSEGSSYPA GTLSWHL D 131

RESULT 6
US-08-432-016-5
; Sequence 5, Application US/08432016
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: ARUFFO, ALEJANDRO
; APPLICANT: PATEL, DHARAKUMAR
; APPLICANT: BOWEN, MICHAEL A.
; APPLICANT: MARQUARDT, HANS
; TITLE OF INVENTION: CD6 LIGAND
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NYXON & VANDERHYE P.C.
; STREET: 110 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/432,016
; FILING DATE: 01-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/333,350
; FILING DATE: 02-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/143,903
; ATTORNEY/AGENT INFORMATION:
; NAME: WILSON, MARY J.
; REGISTRATION NUMBER: 32,955
; REFERENCE/DOCKET NUMBER: 1579-95
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 816-4000
; TELEX/FAX: (703) 816-4100
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-432-016-5

Query Match 51.2%; Score 207; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 5.7e-184;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 AMNRNGKETKSNYRVRVYQIPGKPEIVDSASELTAGVNKGTCVSEGSSYPA GTLSWHL D 160
Db 72 AMNRNGKETKSNYRVRVYQIPGKPEIVDSASELTAGVNKGTCVSEGSSYPA GTLSWHL D 131

RESULT 7
US-08-684-594-5

; Sequence 5, Application US/08684594
; Patent No. 5988172

; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: ARUFO, ALEJANDRO
; APPLICANT: PATEL, DEVALKUMAR
; APPLICANT: BOWEN, MICHAEL A.
; APPLICANT: MARQUARDT, HANS
; TITLE OF INVENTION: CD6 LIGAND
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 NORTH GLEBE ROAD
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: U.S.A.
; ZIP: 22201-4714

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOE/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/684,594
FILING DATE: 18-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/432,016
FILING DATE: 01-MAY-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/333,350
FILING DATE: 02-NOV-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/143,903
FILING DATE: 02-NOV-1993

ATTORNEY/AGENT INFORMATION:
NAME: WILSON, MARY J.
REGISTRATION NUMBER: 32,955
REFERENCE/DOCKET NUMBER: 1579-112

TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100

SEQUENCE CHARACTERISTICS:
LENGTH: 278 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: Protein

Query Match 51.2%; Score 207; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 5.7e-184;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 AMNRNGKETNSNYRVRVYQIPGKPBIVDASSELTAGVNKVGTCVSEGSYPACTLSWHLD 160

Db 72 AMNRNGKETNSNYRVRVYQIPGKPBIVDASSELTAGVNKVGTCVSEGSYPACTLSWHLD 131

Db 161 GKPLVNEKGYSVKETOTRRHPETGLFTLQSELMVTPARGGDPRETFCSFSPGLPRHRL 220

Db 132 GKPLVNEKGYSVKETOTRRHPETGLFTLQSELMVTPARGGDPRETFCSFSPGLPRHRL 191

Qy 221 RTAPIQPRWEPVPLBEVOLVVEPEGGAVAPGGTVTLTCVPAQPSPQIHWMKDGVLPL 280

Db 192 RTAPIQPRWEPVPLBEVOLVVEPEGGAVAPGGTVTLTCVPAQPSPQIHWMKDGVLPL 251

Db 281 PPSPVLLPBPQDQGTYSCVATHSS 307

Db 252 PPSPVLLPBPQDQGTYSCVATHSS 278

RESULT 8
US-09-062-365-5

; Sequence 5, Application US/09062365
; Patent No. 6465422

; GENERAL INFORMATION:
; APPLICANT: Schmidt, Ann Marie
; APPLICANT: Stern, David
; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A
; FILE REFERENCE: 55424
; CURRENT APPLICATION NUMBER: US/09/062,365
; CURRENT FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 6
; SEQ ID NO 5
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Human
; US-09-062-365-5

Query Match 7.4%; Score 30; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.4e-20;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AGNTTARIGEPLVKCKGAPKCPQRLEWK 52

Db 1 AGNTTARIGEPLVKCKGAPKCPQRLEWK 30

RESULT 9
US-08-948-131-1

; Sequence 1, Application US/08948131
; Patent No. 6554651

; GENERAL INFORMATION:
; APPLICANT: Stern, David
; APPLICANT: Yan, Shi Du
; APPLICANT: Schmidt, Ann Marie
; TITLE OF INVENTION: Ligand Binding Site of Rage and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10016

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/948,131

FILING DATE: 09-OCT-1997

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:
NAME: White, John P

Query Match 51.2%; Score 207; DB 2; Length 278;
Best Local Similarity 100.0%; Pred. No. 5.7e-184;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 101 AMNRNGKETNSNYRVRVYQIPGKPBIVDASSELTAGVNKVGTCVSEGSYPACTLSWHLD 160

REGISTRATION NUMBER: 28,678
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-278-0400
 TELEFAX: 212-391-0526
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-09-638-649-1

Query Match 7.4%; Score 30; DB 4; Length 30;
 Best Local Similarity 100.0%; Pred. No. 1.4e-20;
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AQNITARGEPLVJKCKGAKPKEPPRLWK 52
 Db 1 AQNITARGEPLVJKCKGAKPKEPPRLWK 30

RESULT 10
 US-09-638-649-5
 ; Sequence 5, Application US/09638649
 ; Patent No. 6563015
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Yan, Shi Du
 ; TITLE OF INVENTION: GLYCANATION ENPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND NERVE
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: 0575/62175
 ; CURRENT APPLICATION NUMBER: US/09/638,649
 ; CURRENT FILING DATE: 2000-08-14
 ; NUMBER OF SEQ ID NOS: 10
 ; SEQ ID NO 5
 ; SOFTWARE: PatentIn Ver. 2.1
 ; LENGTH: 403
 ; TYPE: PRT
 ; ORGANISM: Murine
 US-09-638-649-5

Query Match 6.4%; Score 26; DB 4; Length 403;
 Best Local Similarity 100.0%; Pred. No. 8.4e-16;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 137 VPNKVGTCVSEGGYPAGTSLWHLDGK 162
 Db 136 VPNKVGTCVSESSYPAGTSLWHLDGK 161

RESULT 11
 US-09-638-649-1
 ; Sequence 1, Application US/09638649
 ; Patent No. 6563015
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Yan, Shi Du
 ; TITLE OF INVENTION: GLYCANATION ENPRODUCT (RAGE) AND MUTANT APP IN BRAIN AND NERVE
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: 0575/62175
 ; CURRENT APPLICATION NUMBER: US/09/638,649
 ; CURRENT FILING DATE: 2000-08-14
 ; NUMBER OF SEQ ID NOS: 10
 ; SEQ ID NO 1
 ; LENGTH: 416
 ; TYPE: PRT

; ORGANISM: Human

RESULT 12
 US-08-755-235-2
 ; Sequence 2, Application US/08755235
 ; Patent No. 6790443
 ; GENERAL INFORMATION:
 ; APPLICANT: Stern, David M.
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Wu, Jun
 ; TITLE OF INVENTION: METHOD FOR TREATING SYMPTOMS OF DIABETES
 ; FILE REFERENCE: 0575/50159
 ; CURRENT APPLICATION NUMBER: US/08/755,235
 ; CURRENT FILING DATE: 1996-11-22
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2
 ; LENGTH: 416
 ; TYPE: PRT
 ; ORGANISM: Bovine
 US-08-755-235-2

Query Match 5.9%; Score 24; DB 4; Length 416;
 Best Local Similarity 100.0%; Pred. No. 6.2e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 237 EVOLVVEPEGGAVAPGGTVLTC 260
 Db 247 EVOLVVEPEGGAVAPGGTVLTC 270

RESULT 13
 US-09-062-365-2
 ; Sequence 2, Application US/09062365
 ; Patent No. 6445422
 ; GENERAL INFORMATION:
 ; APPLICANT: Schmidt, Ann Marie
 ; APPLICANT: Stern, David
 ; TITLE OF INVENTION: METHOD FOR INHIBITING TUMOR INVASION OR SPREADING IN A SUBJECT
 ; FILE REFERENCE: 55424
 ; CURRENT APPLICATION NUMBER: US/09/062,365
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 22
 ; TYPE: PRT
 ; ORGANISM: Human
 US-09-062-365-2

Query Match 5.4%; Score 22; DB 4; Length 22;
 Best Local Similarity 100.0%; Pred. No. 2.9e-13;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGTAGAWVLVLSWGVYVG 22
 Db 1 MAAGTAGAWVLVLSWGVYVG 22

RESULT 14
 US-08-633-148-18
 ; Sequence 18, Application US/08633148

Patent No. 5864018
 GENERAL INFORMATION:
 APPLICANT: MORSE, MICHAEL J.
 APPLICANT: NAGASHIMA, MARIKO
 APPLICANT: HOLLANDER, DORIS A.
 TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
 TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: TOWNSENT & TOWNSENT & CREW LLP
 STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC Compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08/633,148
 FILING DATE: 16-APR-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: MURPHY ESQ., MATTHEW B.
 REGISTRATION NUMBER: 39,787
 REFERENCE/DOCKET NUMBER: 014618-005600US
 TELEPHONE: (415) 326-2422
 TELEFAX: (415) 326-2422
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-633-148-18

Query Match Score 16; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 7.9e-08;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 AQNITARIGEPLVLC 38
 Db 1 AQNITARIGEPLVLC 16

RESULT 15
 US-08-633-148-12
 Sequence 12, Application US/08633148
 GENERAL INFORMATION:
 Patent No. 5864018
 APPLICANT: MORSE, MICHAEL J.
 APPLICANT: NAGASHIMA, MARIKO
 APPLICANT: HOLLANDER, DORIS A.
 TITLE OF INVENTION: ANTIBODIES TO ADVANCED GLYCOSYLATION
 TITLE OF INVENTION: END-PRODUCT RECEPTOR POLYPEPTIDES AND USES THEREFOR
 NUMBER OF SEQUENCES: 23
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: TOWNSENT & TOWNSENT & CREW LLP
 STREET: TWO EMBARCADERO CENTER, 8TH FLOOR
 CITY: SAN FRANCISCO
 STATE: CALIFORNIA
 COUNTRY: U.S.A.
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:

Result No.	Score	Query Match	Length	DB ID	Description
1.	404	100.0	404	1	I61596 advanced Glycosylation end-products receptor precursor - human
2.	26	6.4	402	2	T09062 probable advanced glycosylation end-products receptor precursor - human
3.	24	5.9	416	1	B42879/ S21968 Ig lambda chain -
4.	9	2.2	97	2	S36066 Ig lambda chain -
5.	9	2.2	98	2	S36063 Ig lambda chain -
6.	6	2.2	98	2	S36062 Ig lambda chain -
7.	9	2.2	110	2	S57465 Ig lambda chain V-
8.	9	2.2	112	2	S26555 Ig lambda chain V-
9.	9	2.2	116	2	C27390 Ig lambda chain V-
10.	9	2.2	117	1	LVHT2 Ig lambda chain V-
11.	9	2.2	117	2	S04226 Ig lambda chain V-
12.	9	2.2	120	2	S30528 Ig lambda chain V-
13.	9	2.2	136	2	S42610 Ig lambda chain V-
14.	9	2.2	235	2	S25749 Ig lambda chain -
15.	8	2.0	132	2	C69050 phycyanin alpha
16.	8	2.0	170	2	A87614 pilus assembly protein
17.	8	2.0	267	2	S38617 tetrahymethanoproteins
18.	8	2.0	315	2	T37901 probable purine nucleotide phosphorylase
19.	8	2.0	357	1	KIBBER thymidine kinase (
20.	8	2.0	359	1	KIBBERT probable lipid carrier
21.	8	2.0	394	2	D70674 immunoglobulin homology
22.	8	2.0	401	2	D83873 receptor; immunoglobulin homology
23.	8	2.0	410	2	T13331 transmembrane protein
24.	8	2.0	420	2	T49199 protein homolog
25.	8	2.0	420	2	dnaJ protein homolog
26.	8	2.0	452	2	two component sens
27.	8	2.0	466	2	probable oxidoreductases
28.	8	2.0	549	2	secreted klotho protein
29.	8	2.0	550	2	G70597 disulfide bonds:

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OM protein - protein search, using sw model

Run on: December 6, 2004, 15:08:06 ; Search time 45 Seconds
(without alignments)
863.813 Million cell updates/sec

Title: US-10-069-598-1
Perfect score: 404
Sequence: 1 MAAGTAGAVNLVLISLWGA.....RAELNQSEEPEAGESSTGGP 404

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : PIR 79:
1: Pir1;*
2: Pir2;*
3: Pir3;*
4: Pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

%

Result No.	Score	Query Match	Length	DB ID	Description
1.	404	100.0	404	1	I61596 advanced Glycosylation end-products receptor precursor - human
2.	26	6.4	402	2	T09062 probable advanced glycosylation end-products receptor precursor - human
3.	24	5.9	416	1	B42879/ S21968 Ig lambda chain -
4.	9	2.2	97	2	S36066 Ig lambda chain -
5.	9	2.2	98	2	S36063 Ig lambda chain -
6.	6	2.2	98	2	S36062 Ig lambda chain -
7.	9	2.2	110	2	S57465 Ig lambda chain V-
8.	9	2.2	112	2	S26555 Ig lambda chain V-
9.	9	2.2	116	2	C27390 Ig lambda chain V-
10.	9	2.2	117	1	LVHT2 Ig lambda chain V-
11.	9	2.2	117	2	S04226 Ig lambda chain V-
12.	9	2.2	120	2	S30528 Ig lambda chain V-
13.	9	2.2	136	2	S42610 Ig lambda chain V-
14.	9	2.2	235	2	S25749 Ig lambda chain -
15.	8	2.0	132	2	C69050 phycyanin alpha
16.	8	2.0	170	2	A87614 pilus assembly protein
17.	8	2.0	267	2	S38617 tetrahymethanoproteins
18.	8	2.0	315	2	T37901 probable purine nucleotide phosphorylase
19.	8	2.0	357	1	KIBBER thymidine kinase (
20.	8	2.0	359	1	KIBBERT probable lipid carrier
21.	8	2.0	394	2	D70674 immunoglobulin homology
22.	8	2.0	401	2	D83873 receptor; immunoglobulin homology
23.	8	2.0	410	2	T13331 transmembrane protein
24.	8	2.0	420	2	T49199 protein homolog
25.	8	2.0	420	2	dnaJ protein homolog
26.	8	2.0	452	2	two component sens
27.	8	2.0	466	2	probable oxidoreductases
28.	8	2.0	549	2	secreted klotho protein
29.	8	2.0	550	2	G70597 disulfide bonds:

probable molybdenum protein

hypothetical protein

intermediated film

hypothetical protein

26S proteasome regulatory subunit

membrane klotho protein

hypothetical protein

protein unc-22 (lin-1)

twitchin (similar)

hypothetical protein

ACT domain contain

conserved hypothetical protein

tyrosine kinase group

hypothetical protein

superoxide dismutase

ALIGMENTS

RESULT 1

I61596 advanced glycosylation end-products receptor precursor - human

N:Alternate names: advanced Glycosylation end product-binding protein, 35K; glycoprotein C:Species: Homo sapiens (man)

C:Accession: 161596 #sequence-revision 07-Feb-1997 #text_change 09-Jul-2004 R:Shugaya, K.; Fukagawa, T.; Matsumoto, K.; Mita, K.; Takahashi, E.; Ando, A.; Inoko, H.; Genomics 23, 408-419, 1994

A:Title: Three genes in the human MHC class III region near the junction with the class I interpart of mouse mammary tumor gene int-3.

A:Reference number: A55562; PMID:95137587; PMID:783890

A:Accession: 161596 A:Molecule type: nucleic acid sequence not shown; translation not shown; translated from GB/EMBL A:Residues: 1-404 <RES>

A:Cross-references: UNIPROT:Q15109; GB:D28769; NID:9561657; PID:BAA05958; PID:9561659 R:Nepert, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Pan, Y.C.; Elliston, K.; Ste J. Biol. Chem. 267, 1998-15004, 1992

A:Title: Cloning and expression of a cell surface receptor for advanced glycosylation end-products A:Reference number: A42879; PMID:92340547; PMID:1378843 A:Accession: B42879 A:Molecule type: mRNA A:Residues: 'G', 2-99, 'R', 101-404 <NEE> A:Cross-references: EMBL:W91211; NID:9190845; PID:9190846 A:Experimental source: lung A:Note: sequence extracted from NCBI backbone (NCBIP:109433)

C:Comment: Advanced glycosylation end products are heterogeneous nonenzymatically glycosylated proteins that contribute to tissue lesions in diabetes.

C:Comment: This receptor appears also to mediate the effects of amyloid beta peptide on cells in the neurotoxic pathway that produces dementia in Alzheimer's disease.

C:Genetics:

A:Cross-references: GDB:AGER A:Gene: GDB:AGER A:Map position: 6P0354 / OMIM:600134 A:Introns: 18/1; 53/3; 119/1; 140/3; 170/1; 231/1; 274/3; 322/1; 331/1; 373/2 C:Function: neuronal receptor for amphotericin, a DNA-binding protein involved in neurit C:Superfamily: advanced glycosylation end products receptor; immunoglobulin homology C:Keywords: Alzheimer's disease; Glycoprotein; receptor; transmembrane protein F:1-22/Domain: signal sequence #status Predicted <SIG> F:23-404/Product: advanced glycosylation end products receptor #status Predicted <MAP> F:23-344/Domain: extracellular #status Predicted <EXT> F:31-101/Domain: immunoglobulin homology <IM1> F:137-210/Domain: immunoglobulin homology <IM2> F:25-303/Domain: immunoglobulin homology <IM3> F:345-362/Domain: transmembrane #status Predicted <TM> F:363-404/Domain: intracellular #status Predicted <INT> F:725-81/Binding site: carbohydrate (covalent) #status Predicted F:38-99,144-208,259-301/Disulfide bonds: #status Predicted

Query Match 100.0%; Score 404; DB 1; Length 404;

Best Local Similarity 100.0%; Pred. No. 0; Mismatches 404; Conservative 0; Indels 0; Gaps 0;

1 MAAGTAGAWYLVLISLNGAVQAQNITARIGEPLVILKCGAPPKPBPQLRLEWKLNTRTEA 60
 1 MAAGTAGAWYLVLISLNGAVQAQNITARIGEPLVILKCGAPPKPBPQLRLEWKLNTRTEA 60

Db 1 wKLSPGGPPWDSSARVLPLNSLFLPAVGIODEGIFRCQAMNRNKGKTSNYRVRVQI 120
 1 wKLSPGGPPWDSSARVLPLNSLFLPAVGIODEGIFRCQAMNRNKGKTSNYRVRVQI 120

Qy 61 VPEGGAVAPGGTIVLCEPAQSPQHMKDGYPLPPSPVILIPRIGPDQGTS 300
 61 VPEGGAVAPGGTIVLCEPAQSPQHMKDGYPLPPSPVILIPRIGPDQGTS 300

Db 121 PGKPEIVDSASLTAGYPNKYGTCVSEGSPAGTLSWHLDGKLPVNEKEVSKEOTRH 180
 121 PGKPEIVDSASLTAGYPNKYGTCVSEGSPAGTLSWHLDGKLPVNEKEVSKEOTRH 180

Db 121 PETGLFLQSELMTVTPARGGDRPTFCSFSGLPRLHARLTAPIOPRWPVPLBEVQL 240
 181 PETGLFLQSELMTVTPARGGDRPTFCSFSGLPRLHARLTAPIOPRWPVPLBEVQL 240

Qy 241 VVEPEGGAVALPGGTIVLCEPAQSPQHMKDGYPLPPSPVILIPRIGPDQGTS 300
 241 VVEPEGGAVALPGGTIVLCEPAQSPQHMKDGYPLPPSPVILIPRIGPDQGTS 300

Db 301 CVATHSSHHGPQESRAVSIITIEPGEGETAGSYGSGLGTIALALGIGLGTAAUIGV 360
 301 CVATHSSHHGPQESRAVSIITIEPGEGETAGSYGSGLGTIALALGIGLGTAAUIGV 360

Qy 361 IIWQRQRGERKAPENQEERAILNQSEPEAGESSTGGP 404
 361 IIWQRQRGERKAPENQEERAILNQSEPEAGESSTGGP 404

Db 361 PETGLFLQSELMTVTPARGGDRPTFCSFSGLPRLHARLTAPIOPRWPVPLBEVQL 240

RESULT 2

To 9062
 probable advanced glycosylation end-products receptor precursor - mouse
 N; Alternate names: RAGE
 C; Species: *Mus musculus* (house mouse)
 C; Accession: T09062
 R; Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc
 Submitted to the EMBL Data Library, October 1997
 A; Description: Sequence of the mouse major histocompatibility locus class III region.
 A; Reference number: Z16543
 A; Status: preliminary; translated from GB/EMBL/DBJ
 A; Molecule type: DNA
 A; Residues: 1-402 <ROW>
 A; Cross-references: UNIPROT:O35444; EMBL:AF030001; NID:92564945; PID:92564950

RESULT 4

Query Match Score 5.9%; Score 24; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.2e-14; Indels 0; Gaps 0;

Qy F;1-22/Domain: signal sequence #status predicted <SIG>

F;23-116/Domain: advanced glycosylation end-products receptor RAGE #status predicted <EXT>

F;23-34/Domain: extracellular #status predicted <EXT>

F;31-100/Domain: immunoglobulin homology <IM1>

F;31-209/Domain: immunoglobulin homology <IM2>

F;262-313/Domain: immunoglobulin homology <IM3>

F;355-372/Domain: transmembrane #status predicted <TM>

F;373-416/Domain: intracellular #status predicted <INT>

F;25,80-/Binding site: carbohydrate (Asn) (covalent) #status predicted

F;38-38,143-207,269-311/disulfide bonds: #status predicted

Query Match Score 5.9%; Score 24; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 1.2e-14; Indels 0; Gaps 0;

Qy F;23-237/Domain: carbohydrate (Asn) (covalent) #status predicted

F;247 EVQLVEPEGGAVAPGGTVLTC 270

RESULT 3

Query Match Score 2.2%; Score 9; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.74; Indels 0; Gaps 0;

N; Alternate names: advanced glycosylation end-product-binding protein, 35K; glycoprotein
 C; Species: Bos primigenius taurus (cattle)
 C; Date: 04-Mar-1993 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
 C; Accession: A42879; A2878; S27949
 R; Neerer, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Ban, Y.C.; Elliston, K.; Su

Query Match Score 2.2%; Score 9; DB 2; Length 97;
 Best Local Similarity 100.0%; Pred. No. 0.74; Indels 0; Gaps 0;

N; Alternate names: advanced glycosylation end-product-binding protein, 35K; glycoprotein
 C; Species: Bos primigenius taurus (cattle)
 C; Date: 04-Mar-1993 #sequence revision 07-Feb-1997 #text_change 09-Jul-2004
 R; Neerer, M.; Schmidt, A.M.; Brett, J.; Yan, S.D.; Wang, F.; Ban, Y.C.; Elliston, K.; Su

RESULT 5
 S36063 Ig lambda chain - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1995 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
 C;Accession: S36063
 R;Williams, S.C.
 submitted to the EMBL Data Library, April 1993
 A;Reference number: S36046
 A;Accession: S36063
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-98 <WIL>
 A;Cross-references: EMBL:Z22206; NID:9312866; PIDN:CAA80213.1; PMID:9312866
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin F,15-92;Domain: immunoglobulin homology <IMM>
 Query Match Score 9; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.75%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 251 PGGTVTTC 259
 Db 14 PGGTVTTC 22

RESULT 6
 S36062 Ig lambda chain - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
 C;Accession: S36062
 R;Williams, S.C.
 submitted to the EMBL Data Library, April 1993
 A;Reference number: S36046
 A;Accession: S36062
 A;Molecule type: DNA
 A;Residues: 1-98 <WIL>
 A;Cross-references: EMBL:Z22205; NID:9312865; PIDN:CAA80213.1; PMID:9312866
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin F,15-92;Domain: immunoglobulin homology <IMM>
 Query Match Score 9; DB 2; Length 98;
 Best Local Similarity 100.0%; Pred. No. 0.75%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 251 PGGTVTTC 259
 Db 14 PGGTVTTC 22

RESULT 7
 S57465 Ig lambda chain V-J region - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 21-Jan-2000
 C;Accession: S57465
 R;Patterson, G.; Wilson, G.; Kennedy, P.G.E.; Willison, H.J.
 A;Description: Analysis of anti-GM1 ganglioside IgM antibodies cloned from motor neurons
 A;Reference number: S57408
 A;Accession: S57465
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-110 <PAT>
 A;Cross-references: EMBL:X87896; NID:9871390; PIDN:CAA61147.1; PMID:9871391
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 F,15-92;Domain: immunoglobulin homology <IMM>
 Query Match Score 9; DB 2; Length 110;

Best Local Similarity 100.0%; Pred. No. 0.83%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 251 PGGTVTTC 259
 Db 14 PGGTVTTC 22

RESULT 8
 S26655 Ig lambda chain V region (hybridoma CH4-14) - chimpanzee (fragment)
 C;Species: Pan troglodytes (chimpanzee)
 C;Date: 19-Mar-1997 #sequence_revision 18-Jul-1997 #text_change 21-Jan-2000
 C;Accession: S26655
 R;Bhririch, P.H.; Mousatova, Z.A.; Harfeldt, K.B.; Isaacson, C.; Oestberg, L.
 Hum. Antibodies Hybridomas 1, 23-26, 1990
 A;Title: Potential of primate monoclonal antibodies to substitute for human antibodies: I
 A;Reference number: S26655
 A;Accession: S26655
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-112 <EBE>
 A;Cross-references: RNBL:Z65288
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: immunoglobulin F,15-92;Domain: immunoglobulin homology <IMM>
 Query Match Score 9; DB 2; Length 112;
 Best Local Similarity 100.0%; Pred. No. 0.84%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 251 PGGTVTTC 259
 Db 14 PGGTVTTC 22

RESULT 9
 C27390 Ig lambda chain precursor V region - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 21-Jan-2000
 C;Accession: C27390
 R;Steen, M.L.; Hellmann, L.; Pettersson, U.
 Gene 55, 75-84, 1987
 A;Title: The immunoglobulin lambda locus in rat consists of two C-lambda genes and a single
 A;Reference number: A27390; PMID:87305594; PMID:3114047
 A;Accession: C27390
 A;Molecule type: DNA
 A;Residues: 1-116 <STE>
 A;Cross-references: GB:MI17092; NID:9204880; PIDN:AAA41423.1; PMID:9204881
 C;Genetics:
 A;Introns: 15/3
 C;Superfamily: immunoglobulin V region; immunoglobulin F,34-111;Domain: immunoglobulin homology <IMM>
 Query Match Score 9; DB 2; Length 116;
 Best Local Similarity 100.0%; Pred. No. 0.86%;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 251 PGGTVTTC 259
 Db 33 PGGTVTTC 41

RESULT 10
 LTHU2 Ig lambda chain precursor V region (4A) - human
 C;Species: Homo sapiens (man)
 C;Date: 04-Dec-1996 #sequence_revision 04-Dec-1996 #text_change 09-Jul-2004
 C;Accession: A01993; S36061
 R;Anderson, M.L.M.; Szajnert, M.F.; Kaplan, J.C.; McColl, L.; Young, B.D.
 Nucleic Acids Res. 12, 6647-6661, 1984

A;Title: The isolation of a human Ig V-lambda gene from a recombinant library of chromosomes
 A;Reference number: A01933; MUID:85014122; PMID:6091030

A;Accession: A01933

A;Molecule type: DNA

A;Residues: 1-117 <ND>

A;Cross-references: UNIPROT:PO4211

A;Note: the sequence was determined from the germline gene

R;Williams, S.C.

Submitted to the EMBL Data Library, April 1993

A;Reference number: S36046

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 21-117 <WIL>

A;Cross-references: EMBL:222204; NID:9312869; PIDN:CAA80212_1; PID:g312870

C;Genetics:

A;Gene: DBP; IGLV@

A;Cross-references: GDB:119342; OMIM:147240

A;Map Position: 2q11.-2q11.2

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kag) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into large superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-20/Domain: signal sequence #status predicted <SIG>

F;21-117/Product: Ig lambda chain V region (AA) #status predicted <MAT>

F;35-112/Domain: immunoglobulin homology <IMM>

F;43-5/Region: complementarity-determining 1

F;56-71/Region: framework 2

F;72-78/Region: complementarity-determining 2

F;79-110/Region: framework 3

F;111-117/Region: complementarity-determining 3

F;42-110/Dissulfide bonds: #status predicted

A;Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup

A;Reference number: S04525; MUID:89282401; PMID:249871

A;Accession: S04526

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-117 <ALE>

A;Cross-references: EMBL:X14614; NID:933406; PIDN:CAA32268_1; PID:g9736247

C;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>

F;34-111/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 9; DB 2; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.87; Mismatches 0; Indels 0; Gaps 0;

Db 34 PGGTVTTC 42

RESULT 11

S04526

Ig lambda chain precursor V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 21-Jan-2000

C;Accession: S04526

R;Alexandre, D.; Chuchana, P.; Brockly, F.; Blancher, A.; Lefranc, G.; Lefranc, M.P.

Nucleic Acids Res. 17, 3975, 1989

A;Title: First genomic sequence of a human Ig variable lambda gene belonging to subgroup

A;Reference number: S04525; MUID:89282401; PMID:249871

A;Accession: S04526

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-117 <ALE>

A;Cross-references: EMBL:X14614; NID:933406; PIDN:CAA32268_1; PID:g9736247

C;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1989

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology <IMM>

F;34-111/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 9; DB 2; Length 117;

Best Local Similarity 100.0%; Pred. No. 0.87; Mismatches 0; Indels 0; Gaps 0;

Db 33 PGGTVTTC 41

RESULT 12

S30528

Ig lambda chain V region - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000

C;Accession: S30528

R;Mariette, X.

Submitted to the EMBL Data Library, October 1992

A;Reference number: S30520

A;Accession: S30528

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-120 <XAR>

A;Cross-references: EMBL:Z18334

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-32/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 9; DB 2; Length 120;

Best Local Similarity 100.0%; Pred. No. 0.89; Mismatches 0; Indels 0; Gaps 0;

Db 14 PGGTVTTC 22

RESULT 13

S42610

ARMVlambda protein precursor - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Sep-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S42610

R;Spatz, L.A.; Williams, M.; Bredner, B.; Desai, R.; Latov, N.

J. Neuroimmunol. 36, 29-39, 1992

A;Title: DNA sequence analysis and comparison of the variable heavy and light chain regions of the IgM lambda chain precursor protein

A;Reference number: S42610; MUID:92138794; PMID:1370957

A;Accession: S42610

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-136 <SPA>

A;Cross-references: EMBL:X54136; PID:9433485; PMID:9433486

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;39-116/Domain: immunoglobulin homology <IMM>

Query Match 2.2%; Score 9; DB 2; Length 136;

Best Local Similarity 100.0%; Pred. No. 0.99; Mismatches 0; Indels 0; Gaps 0;

Db 38 PGGTVTTC 259

RESULT 14

S25749

Ig lambda chain - human

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S25749

R;Combiato, G.; Klobbeck, H.G.

Bur. J. Immunol. 21, 1513-1522, 1991

A;Title: Vlambda1 and Jlambda1 genes segments of the human immunoglobulin lambda chain

A;Reference number: S16439; MUID:91257162; PMID:1370957

A;Accession: S25749

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-235 <COM>

A;Cross-references: EMBL:X57814; PID:93327; PMID:CAA4051_1; PMID:933728

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;150-218/Domain: immunoglobulin homology <IMM>

Query Match Score 9; DB 2; Length 235;
 Best Local Similarity 100.0%; Pred. No. 1.6;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 251 PGGRVTLTC 259
 Db 33 PGGRVTLTC 41

RESULT 15

C69050 phycocyanin alpha phycocyanobilin lyase CpcE - Methanobacterium thermoautotrophicum (str C; species: Methanobacterium thermoautotrophicum

C; Accession: C69050 C; Date: 05-JEC-1997 #sequence_change 05-Dec-1997 #text_change 09-Jul-2004

R; Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldridge, T.;
 Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwanji, N.;
 ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.

J. Bacteriol. 179, 7135-7155, 1997.

A; Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct

A; Reference number: A69000; MUID:98037514; PMID:9374463

A; Status: preliminary; nucleic acid sequence not shown; translation not shown

A; Molecule type: DNA

A; Residues: 1-132 <MTH>

A; Cross-references: UNIPROT:Q27431; GB:AE000901; GB:AE000666; NID:92622486; PIDN:AAB8585

A; Experimental source: strain Delta H

A; Gene: MTH1378

A; Start codon: GTG

Query Match Score 8; DB 2; Length 132;
 Best Local Similarity 100.0%; Pred. No. 8.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 342 ALAIGILG 349
 Db 90 ALAIGILG 97

Search completed: December 6, 2004, 15:18:36
 Job time : 48 secs



DE Soluble form of receptor for advanced glycation endproducts
precursor.

DE Name=RAGE;

OS Homo sapiens (Human). Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

RN [1]

SEQUENCE FROM N.A.

TISSUE=Skin;

RC MEDLINE=12495433; PubMed=12495433;

RX RX

RA Yonekura H., Yamamoto Y., Sakurai S., Petrova R.G., Abedin Md. J.,

RA Li H., Yasui K., Takeuchi M., Makita Z., Takasawa S., Okamoto H.,

RA Watanabe T., Yamamoto H.;

RT "Novel splice variants of the receptor for advanced glycation end-products expressed in human vascular endothelial cells and pericytes, and their putative roles in diabetes-induced vascular injury.";

RL Biochem. J. 370:1097-1109 (2003).

DR EMBL; AB01668; BRCS5455.1; -.

DR InterPro; IP004872; F:receptor activity; IEA.

DR InterPro; IPR003598; Ig-like.

DR InterPro; IPR003006; Ig_C2.

DR SMART; SM00408; IgC2; 1.

DR PROSITE; PS50835; Ig_LIKE; 1.

DR PROSITE; PS00290; Ig_MHC; UNKNOWN_1.

KW Receptor.

FT NON_TER 1

SQ SEQUENCE 147 AA; 15676 MW; F4D9D530B2EAC934 CRC64;

Query Match 32.4%; Score 131; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 6. 4e-18;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 DPRPTFSCSFSPGLPRLRALTAPIQPRVWEPVPLEVQLVVEPEGGAVAPGGTVTLTCB 260
FT 1 DPRPTFSCSFSPGLPRLRALTAPIQPRVWEPVPLEVQLVVEPEGGAVAPGGTVTLTCB 60

DB 261 VPAQPSQIHWMDGVPVLPLPPSPVLLPEIPIGPODGTYSCVATHSHGPQESRAVSI 320
SQ SIGNAL 1 22
SEQUENCE 347 AA; 37050 MW; 519E377C4D6AC62C CRC64;

QY 61 VPAQPSQIHWMDGVPVLPLPPSPVLLPEIPIGPODGTYSCVATHSHGPQESRAVSI 120
FT 1 MAAGTAVGAWLVYLSLWGAVGAAONITARIGEPLVVKCKGAKPKPPOLEWKLNTRGRTEA 60
DB 1 MAAGTAVGAWLVYLSLWGAVGAAONITARIGEPLVVKCKGAKPKPPOLEWKLNTRGRTEA 60
QY . 61 WKVLSPOGGPWDSVARVLPGNSLFLPAGVQDDEGIFRCQAMNRNGKETKSNTYRVYQI 120
DB 61 WKVLSPOGGPWDSVARVLPGNSLFLPAGVQDDEGIFRCQAMNRNGKETKSNTYRVYQI 120
QY . 121 PGKEPEIVDSSAELTAGVNKGTCVSEGSSYPAGTLSWHDGKLPVNGKVSYKEQTRH 180
DB 121 PGKEPEIVDSSAELTAGVNKGTCVSEGSSYPAGTLSWHDGKLPVNGKVSYKEQTRH 180
QY 181 PETGLFTLQSELMVTPARCGDPRTFSCSFSPGLPRLRALTAPIQPRVWEPVPLEEVOL 240
DB 181 PETGLFTLQSELMVTPARCGDPRTFSCSFSPGLPRLRALTAPIQPRVWEPVPLEEVOL 240
QY 241 VVEPEGGAVAPGGSYTLLICEVPAQSPQTHWMKDGVPLPLPPSPVLLPEIPIGPODGTY 300
DB 241 VVEPEGGAVAPGGSYTLLICEVPAQSPQTHWMKDGVPLPLPPSPVLLPEIPIGPODGTY 300
QY 301 CVATHSHGPQESRAVSI1IPEEGPTAG 331
DB 301 CVATHSHGPQESRAVSI1IPEEGPTAG 331

RESULT 3

Q71BG7 PRELIMINARY;

AC Q71BG7 PRELIMINARY;

DT 05-JUL-2004 (TREMBLe1. 27, Created)

DT 05-JUL-2004 (TREMBLe1. 27, Last sequence update)

DE Advanced glycosylation end product-specific receptor variant sRAGE2
(Fragment).

GN Name=AGBR;

OS Homo sapiens (Human).

RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

RN [1]

SEQUENCE FROM N.A.

FT NON_TER 1

SQ SEQUENCE 147 AA; 15676 MW; F4D9D530B2EAC934 CRC64;

Query Match 32.4%; Score 131; DB 2; Length 147;
Best Local Similarity 100.0%; Pred. No. 6. 4e-18;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 201 DPRPTFSCSFSPGLPRLRALTAPIQPRVWEPVPLEVQLVVEPEGGAVAPGGTVTLTCB 260
DB 1 DPRPTFSCSFSPGLPRLRALTAPIQPRVWEPVPLEVQLVVEPEGGAVAPGGTVTLTCB 60

Qy	261 VPAQPSPOIHHMKDGYPLPPLPPSPVNLILPEIGPQDGTYSCVATHSSHPQESRAVSI ;	FT	NON-TER	1	1	
Db	61 VPAQPSPOIHHMKDGYPLPPLPPSPVNLILPEIGPQDGTYSCVATHSSHPQESRAVSI ;	SQ	SEQUENCE	50 AA;	5708 MW;	71A023326D84ADD9C CRC64 ;
Qy	321 IEPGEEGPTAG 331	Query Match	7.4%;	Score 30;	DB 2;	Length 50;
Db	121 IEPGEEGPTAG 131	Best Local Similarity	100.0%;	Pred. No. 1.2e-20;		
		Matches	30;	Conservative	0;	Mismatches
Qy	201 DPRPTFCSFSFGPLPRHRLTAPIQPRVW 230	Qy	201 DPRPTFCSFSFGPLPRHRLTAPIQPRVW 230	Indels	0;	Gaps
Db	1 DFRPTFCSFSFGPLPRHRLTAPIQPRVW 30	Db	1 DFRPTFCSFSFGPLPRHRLTAPIQPRVW 30			
RESULT 5						
Q9UQR5	PRELIMINARY;	PRT;	82 AA.			
ID	Q9UQR5					
AC						
DT	01-MAY-2000 (TREMBLrel. 13, Created)	ID	AAQ10685	PRELIMINARY;	PRT;	50 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	ID	AAQ10685,			
DT	01-MAY-2001 (TREMBLrel. 19, Last annotation update)	AC				
DE	Receptor for advanced glycosylation end product (FrAGMENT).	DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)			
GN	Name=RAGE;	DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)			
GN	Homo sapiens (Human).	DE	Advanced Glycosylation end product-specific receptor variant sRAGE1			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DE	(Fragment).			
OC	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	DE	Advanced Glycosylation end product-specific receptor variant sRAGE1			
RA	RANKOVA K.; SEQUENCE FROM N.A.	DE	(Fragment).			
RN	[1]	GN	AGER.			
RP	NCBI_TAXID=9606;	RN				
RA	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.	RP	SEQUENCE FROM N.A.			
DR	EMBL; AJ238896; CAB43094.1; -.	RX	Medline=22941919; PubMed=14580673;			
DR	GO; GO:0004872; F:receptor activity; IEA.	RA	Schlueter C.; Hauke S., Flöhr A.M., Rogalla P., Bullerdiek J.;			
KW	Receptor.	RT	"Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";			
FT	NON-TER	RT	Biochim. Biophys. Acta 1630:1-6(2003).			
SQ	SEQUENCE 82 AA; 8423 MW; 06D81F3634AD38F8 CRC64 ;	RL	DR EMBL; AF536236; AAQ10685.1; -.			
RA	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.	RN	NCBI_TAXID=9606;			
DR	EMBL; AJ238896; CAB43094.1; -.	RP	SEQUENCE FROM N.A.			
DR	GO; GO:0004872; F:receptor activity; IEA.	RX	Medline=22941919; PubMed=14580673;			
KW	Receptor.	RA	Schlueter C.; Hauke S., Flöhr A.M., Rogalla P., Bullerdiek J.;			
FT	NON-TER	RT	"Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";			
SQ	SEQUENCE 82 AA; 8423 MW; 06D81F3634AD38F8 CRC64 ;	RL	Biochim. Biophys. Acta 1630:1-6(2003).			
RESULT 7						
Q9UQR5	PRELIMINARY;	PRT;	82 AA.			
ID	Q9UQR5					
AC						
DT	01-MAY-2000 (TREMBLrel. 13, Created)	ID	AAQ10685	PRELIMINARY;	PRT;	50 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	ID	AAQ10685,			
DT	01-MAY-2001 (TREMBLrel. 19, Last annotation update)	AC				
DE	Receptor for advanced glycosylation end product (FrAGMENT).	DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)			
GN	Name=RAGE;	DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)			
GN	Homo sapiens (Human).	DE	Advanced Glycosylation end product-specific receptor variant sRAGE1			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DE	(Fragment).			
OC	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	DE	Advanced Glycosylation end product-specific receptor variant sRAGE1			
RA	RANKOVA K.; SEQUENCE FROM N.A.	DE	(Fragment).			
RN	[1]	GN	AGER.			
RP	NCBI_TAXID=9606;	RN				
RA	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.	RP	SEQUENCE FROM N.A.			
DR	EMBL; AJ238896; CAB43094.1; -.	RX	Medline=22941919; PubMed=14580673;			
DR	GO; GO:0004872; F:receptor activity; IEA.	RA	Schlueter C.; Hauke S., Flöhr A.M., Rogalla P., Bullerdiek J.;			
KW	Receptor.	RT	"Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";			
FT	NON-TER	RL	Biochim. Biophys. Acta 1630:1-6(2003).			
SQ	SEQUENCE 82 AA; 8423 MW; 06D81F3634AD38F8 CRC64 ;	RN	NCBI_TAXID=9606;			
RESULT 8						
Q9UQR5	PRELIMINARY;	PRT;	82 AA.			
ID	Q9UQR5					
AC						
DT	05-JUL-2004 (TREMBLrel. 27, Created)	ID	AAQ10782	PRELIMINARY;	PRT;	50 AA.
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	ID	AAQ10782;			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	AC				
DE	Advanced Glycosylation end product-specific receptor RAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)			
DE	Glycosylation end product-specific receptor variant sRAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)			
DE	Glycosylation end product-specific receptor variant sRAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DE	Advanced Glycosylation end product-specific receptor RAGE3			
DE	Glycosylation end product-specific receptor variant sRAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DE	(Fragment).			
GN	Name=AGER;	DE	Advanced Glycosylation end product-specific receptor RAGE3			
GN	Homo sapiens (Human).	DE	(Fragment).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DE	Advanced Glycosylation end product-specific receptor RAGE3			
OC	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	DE	(Fragment).			
RA	RANKOVA K.; SEQUENCE FROM N.A.	DE	Advanced Glycosylation end product-specific receptor RAGE3			
RN	[1]	GN	AGER.			
RP	NCBI_TAXID=9606;	RN				
RA	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.	RP	SEQUENCE FROM N.A.			
DR	EMBL; AJ238896; CAB43094.1; -.	RX	Medline=22941919; PubMed=14580673;			
DR	GO; GO:0004872; F:receptor activity; IEA.	RA	Schlueter C.; Hauke S., Flöhr A.M., Rogalla P., Bullerdiek J.;			
KW	Receptor.	RT	"Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";			
FT	NON-TER	RL	Biochim. Biophys. Acta 1630:1-6(2003).			
SQ	SEQUENCE 82 AA; 8423 MW; 06D81F3634AD38F8 CRC64 ;	RN	NCBI_TAXID=9606;			
RESULT 6						
Q71BB6	PRELIMINARY;	PRT;	50 AA.			
ID	Q71BB6					
AC						
DT	05-JUL-2004 (TREMBLrel. 27, Created)	ID	AAQ10782	PRELIMINARY;	PRT;	50 AA.
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	ID	AAQ10782;			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	AC				
DE	Advanced Glycosylation end product-specific receptor RAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)			
DE	Glycosylation end product-specific receptor variant sRAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)			
DE	Glycosylation end product-specific receptor variant sRAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DE	Advanced Glycosylation end product-specific receptor RAGE3			
DE	Glycosylation end product-specific receptor variant sRAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DE	(Fragment).			
GN	Name=AGER;	DE	Advanced Glycosylation end product-specific receptor RAGE3			
GN	Homo sapiens (Human).	DE	(Fragment).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DE	Advanced Glycosylation end product-specific receptor RAGE3			
OC	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	DE	(Fragment).			
RA	RANKOVA K.; SEQUENCE FROM N.A.	DE	Advanced Glycosylation end product-specific receptor RAGE3			
RN	[1]	GN	AGER.			
RP	NCBI_TAXID=9606;	RN				
RA	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.	RP	SEQUENCE FROM N.A.			
DR	EMBL; AJ238896; CAB43094.1; -.	RX	Medline=22941919; PubMed=14580673;			
DR	GO; GO:0004872; F:receptor activity; IEA.	RA	Schlueter C.; Hauke S., Flöhr A.M., Rogalla P., Bullerdiek J.;			
KW	Receptor.	RT	"Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";			
FT	NON-TER	RL	Biochim. Biophys. Acta 1630:1-6(2003).			
SQ	SEQUENCE 82 AA; 8423 MW; 06D81F3634AD38F8 CRC64 ;	RN	NCBI_TAXID=9606;			
RESULT 5						
Q9UQR5	PRELIMINARY;	PRT;	82 AA.			
ID	Q9UQR5					
AC						
DT	01-MAY-2000 (TREMBLrel. 13, Created)	ID	AAQ10685	PRELIMINARY;	PRT;	50 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	ID	AAQ10685;			
DT	01-MAY-2001 (TREMBLrel. 19, Last annotation update)	AC				
DE	Receptor for advanced glycosylation end product (FrAGMENT).	DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)			
GN	Name=RAGE;	DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)			
GN	Homo sapiens (Human).	DE	Advanced Glycosylation end product-specific receptor variant sRAGE1			
OC	Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.	DE	(Fragment).			
RA	RANKOVA K.; SEQUENCE FROM N.A.	DE	Advanced Glycosylation end product-specific receptor variant sRAGE1			
RN	[1]	GN	AGER.			
RP	NCBI_TAXID=9606;	RN				
RA	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.	RP	SEQUENCE FROM N.A.			
DR	EMBL; AJ238896; CAB43094.1; -.	RX	Medline=22941919; PubMed=14580673;			
DR	GO; GO:0004872; F:receptor activity; IEA.	RA	Schlueter C.; Hauke S., Flöhr A.M., Rogalla P., Bullerdiek J.;			
KW	Receptor.	RT	"Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";			
FT	NON-TER	RL	Biochim. Biophys. Acta 1630:1-6(2003).			
SQ	SEQUENCE 82 AA; 8423 MW; 06D81F3634AD38F8 CRC64 ;	RN	NCBI_TAXID=9606;			
RESULT 6						
Q71BB6	PRELIMINARY;	PRT;	50 AA.			
ID	Q71BB6					
AC						
DT	05-JUL-2004 (TREMBLrel. 27, Created)	ID	AAQ10782	PRELIMINARY;	PRT;	50 AA.
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)	ID	AAQ10782;			
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)	AC				
DE	Advanced Glycosylation end product-specific receptor RAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)			
DE	Glycosylation end product-specific receptor variant sRAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)			
DE	Glycosylation end product-specific receptor variant sRAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DE	Advanced Glycosylation end product-specific receptor RAGE3			
DE	Glycosylation end product-specific receptor variant sRAGE3 (Advanced Glycosylation end product-specific receptor variant sRAGE3)	DE	(Fragment).			
GN	Name=AGER;	DE	Advanced Glycosylation end product-specific receptor RAGE3			
GN	Homo sapiens (Human).	DE	(Fragment).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	DE	Advanced Glycosylation end product-specific receptor RAGE3			
OC	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	DE	(Fragment).			
RA	RANKOVA K.; SEQUENCE FROM N.A.	DE	Advanced Glycosylation end product-specific receptor RAGE3			
RN	[1]	GN	AGER.			
RP	NCBI_TAXID=9606;	RN				
RA	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.	RP	SEQUENCE FROM N.A.			
DR	EMBL; AJ238896; CAB43094.1; -.	RX	Medline=22941919; PubMed=14580673;			
DR	GO; GO:0004872; F:receptor activity; IEA.	RA	Schlueter C.; Hauke S., Flöhr A.M., Rogalla P., Bullerdiek J.;			
KW	Receptor.	RT	"Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";			
FT	NON-TER	RL	Biochim. Biophys. Acta 1630:1-6(2003).			
SQ	SEQUENCE 82 AA; 8423 MW; 06D81F3634AD38F8 CRC64 ;	RN	NCBI_TAXID=9606;			
RESULT 7						
Q9UQR5	PRELIMINARY;	PRT;	82 AA.			
ID	Q9UQR5					
AC						
DT	01-MAY-2000 (TREMBLrel. 13, Created)	ID	AAQ10685	PRELIMINARY;	PRT;	50 AA.
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	ID	AAQ10685;			
DT	01-MAY-2001 (TREMBLrel. 19, Last annotation update)	AC				
DE	Receptor for advanced glycosylation end product (FrAGMENT).	DT	02-MAR-2004 (TREMBLrel. 27, Last sequence update)			
GN	Name=RAGE;	DT	02-MAR-2004 (TREMBLrel. 27, Last annotation update)			
GN	Homo sapiens (Human).	DE	Advanced Glycosylation end product-specific receptor variant sRAGE1			
OC	Eukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.	DE	(Fragment).			
RA	RANKOVA K.; SEQUENCE FROM N.A.	DE	Advanced Glycosylation end product-specific receptor variant sRAGE1			
RN	[1]	GN	AGER.			
RP	NCBI_TAXID=9606;	RN				
RA	Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.	RP	SEQUENCE FROM N.A.			
DR	EMBL; AJ238896; CAB43094.1; -.	RX	Medline=22941919; PubMed=14580673;			
DR	GO; GO:0004872; F:receptor activity; IEA.	RA	Schlueter C.; Hauke S., Flöhr A.M., Rogalla P., Bullerdiek J.;			
KW	Receptor.	RT	"Tissue-specific expression patterns of the RAGE receptor and its soluble forms-a result of regulated alternative splicing?";			
FT	NON-TER	RL	Biochim. Biophys. Acta 1630:1-6(2003).			
SQ	SEQUENCE 82 AA; 8423 MW; 06D81F3634AD38F8 CRC64 ;	RN	NCBI_TAXID=9606;			

Query Match	7.4%;	Score 30;	DB 2;	Length 50;		
Best Local Similarity	100.0%;	Pred. No. 1.2e-20;				
Matches	30;	Conservative	0;	Mismatches	0;	
Qy	201 DPPRTFSCSFSPGLPRHRALETTAPIQRWV	230				
Db	1 DERPTFSCSFSPGLPRHRALETTAPIQRWV	30				
RESULT 9						
RAGE_RAT	RAGE_RAT	STANDARD;	PRT;	402 AA.		
AC	Q63475;					
DT	01-NOV-1997 (Rel. 35, Created)					
DT	01-NOV-1997 (Rel. 35, Last sequence update)					
DE	Advanced Glycosylation end product-specific receptor precursor (Receptor for advanced glycosylation end products).					
GN	Name=Ager; Synonyms=Rage;					
OS	Rattus norvegicus (Rat).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
OX	NCBI_TaxID=10116;					
RN	[1]					
SEQUENCE FROM N.A.						
RC	SEQUENCE FROM N.A.					
RX	STRAIN=Sprague-Dawley; TISSUE=Lung;					
RX	MEDLINE=91368045; PubMed=922412;					
RA	Renard C., Chappé O., Wautier M.P., Nagashima M., Lundh E., Morber J., Zhao J., Schmid A.M., Schermann J.M., Wautier J.L.; RT "Recombinant advanced glycation end product receptor pharmacokinetics in normal and diabetic rats."					
RL	Mol. Pharmacol. 52:54-62(1997).					
CC	-!- FUNCTION: Mediates interactions of advanced glycosylation end products (AGE). These are nonenzymatically glycosylated proteins which accumulate in vascular tissue in aging and at an accelerated rate in diabetes.					
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.					
CC	-!- TISSUE SPECIFICITY: Endothelial cells.					
CC	-!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.					
CC	-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.					
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).					
EMBL; RGD; 692548; Ager.	AAA42027.1;	-.				
DR	InterPro; IPR007110; Ig-like.					
DR	InterPro; IPR003598; Ig_C2.					
DR	Pfam; PF00047; ig_3.					
DR	SMART; SM00408; IgG2; 1.					
DR	PROSITE; PS50835; Ig_LIKE; 3.					
DR	PROSITE; PS00290; Ig_MHC; 1.					
DR	Glycoprotein; Immunoglobulin domain; Repeat; Signal; Transmembrane.					
FT	SIGNAL 1	22	Potential.			
FT	CHAIN 23	402	Advanced glycosylation end product-specific receptor.			
FT	DOMAIN 23	341	Extracellular (Potential).			
FT	TRANSMEM 342	362	Potential.			
FT	DOMAIN 353	402	Cytoplasmic (Potential).			
FT	DOMAIN 23	109	Ig-like V-type.			
FT	DOMAIN 123	219	Ig-like C2-type 1.			
FT	DOMAIN 233	315	Ig-like C2-type 2.			
FT	DISULFID 38	98	Potential.			
FT	DISULFID 143	206	Potential.			
FT	CARBOHYD 259	25	Potential.			
FT	CARBOHYD 25	25	N-linked (GlcNAc- . .) (Potential).			
RESULT 10						
QY	137 VPNVKGTCVSEGSPAGTLISWHLDGKPL	164				
Db	136 VPNVKGTCVSEGSPAGTLISWHLDGKPL	163				
SEQUENCE FROM N.A.						
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Brown Norway;					
RX	PubMed=15060004;					
RA	Hurt P., Sudbrak R., Klages S., Mueller I., Shihna T., Inoko H., Lehrach H., Reinhardt R., Himmelbauer H., "The genomic sequence and comparative analysis of the rat major histocompatibility complex." Genome Res. 14:631-639(2004).					
RL	[1]					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Brown Norway;					
RA	Boehm S., Borzym K., Gelling S., Gimmler V., Heitmann K., Koslura A., Lang N., Lehrack S., Sontag M., Hurt P., Himmelbauer H., "The genomic sequence and comparative analysis of the rat major histocompatibility complex." Genome Res. 14:631-639(2004).					
RL	[2]					
DR	B88304; CABE83960.1; -.					
DR	GO: GO0004812; F: receptor activity; IEA.					
DR	InterPro; IPR033599; Ig.					
DR	InterPro; IPR007110; Ig-1-like.					
DR	InterPro; IPR003588; Ig_C2.					
DR	InterPro; IPR003006; Ig_MHC.					
DR	PFAM; PF00047; Ig_3.					
DR	SMART; SM00408; IGC2; 2.					
DR	PROSITE; PS50835; Ig_LIKE; 3.					
DR	PROSITE; PS00290; Ig_MHC; UNKNOWN_1.					
DR	Receptor.					
SQ	SEQUENCE 402 AA;	42644 MW;	CEA49453C05B1CA1 CRC64;			
QY	137 VPNVKGTCVSEGSPAGTLISWHLDGKPL	164				
Db	136 VPNVKGTCVSEGSPAGTLISWHLDGKPL	163				
RESULT 11						
QY	137 VPNVKGTCVSEGSPAGTLISWHLDGKPL	164				
Db	136 VPNVKGTCVSEGSPAGTLISWHLDGKPL	163				
SEQUENCE FROM N.A.						
RP	SEQUENCE FROM N.A.					
RC	STRAIN=Brown Norway;					
RA	CABE83960; CABE83960.					
RA	InterPro; IPR007110; Ig-1-like.					
RA	InterPro; IPR003598; Ig_C2.					
RA	PFAM; PF00047; ig_3.					
RA	SMART; SM00408; IgG2; 1.					
RA	PROSITE; PS50835; Ig_LIKE; 3.					
RA	PROSITE; PS00290; Ig_MHC; 1.					
RA	Glycoprotein; Immunoglobulin domain; Repeat; Signal; Transmembrane.					
FT	SIGNAL 1	22	Potential.			
FT	CHAIN 23	402	Advanced glycosylation end product-specific receptor.			
FT	DOMAIN 23	341	Extracellular (Potential).			
FT	TRANSMEM 342	362	Potential.			
FT	DOMAIN 353	402	Cytoplasmic (Potential).			
FT	DOMAIN 23	109	Ig-like V-type.			
FT	DOMAIN 123	219	Ig-like C2-type 1.			
FT	DOMAIN 233	315	Ig-like C2-type 2.			
FT	DISULFID 38	98	Potential.			
FT	DISULFID 143	206	Potential.			
FT	CARBOHYD 259	25	N-linked (GlcNAc- . .) (Potential).			
FT	CARBOHYD 25	25	AGPR			

OS	Rattus norvegicus (Rat).	RA	Jones S.J., Marra M.A.;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi.	RT	"Generation and initial analysis of more than 15,000 full-length human
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	RT	and mouse cDNA sequences";
OX	NCBI_TaxID=10116;	RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[1]	RN	
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	STRAIN=Brown Norway;	RC	Strausberg R.;
RA	Hurt P., Walter L., Sudbrak R., Klages S., Mueller I., Shiraia T.,	RA	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
RA	Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosciura A.,	RL	[3]
RA	Lang N., Lehrack H., Guenther E., Reinhardt R., Himmelbauer H.,	DR	EMBL; AF03001; AAB82007.1;
RA	Sudbrak R., Reinhart R.;	DR	EMBL; BC061182; AAH61182.1;
RL	Submitted (DBC-2003) to the EMBL/GenBank/DBJ databases.	DR	PTR; T09062; T09062.
DR	DRBML; BX83044; CAE83960.1.; -.	DR	GO; GO:0004872; F:receptor activity; IEA.
KW	Receptor.	DR	InterPro; IPR00110; Ig-like.
RC	STRAIN-Brown Norway;	DR	InterPro; IPR003598; Ig_C2.
RA	Boehm S., Borzym K., Gelling S., Gimmel V., Heitmann K., Kosciura A.,	DR	InterPro; IPR003006; Ig_MHC.
RA	Lang N., Lehrack H., Thiel J., Sonteg M., Hurt P., Himmelbauer H.,	DR	Pfam; PF00047; Ig_2.
RA	Sudbrak R., Reinhart R.;	DR	SMART; SM00408; IgC2_1.
RL	Submitted (DBC-2003) to the EMBL/GenBank/DBJ databases.	DR	PROSITE; PS50835; Ig_LIKE; 3.
DR	DRBML; BX83044; CAE83960.1.; -.	DR	PROSITE; PS00290; Ig_MHC; UNKNOWN_1.
KW	Receptor.	DR	Receptor.
SQ	SEQUENCE FROM N.A.	SQ	SEQUENCE 402 AA; 42653 MW; DBFDC50A6C8CB902 CRC64;
Query Match	6.9%	Query Match	6.4%; Score 26; DB 2; Length 402;
Best Local Similarity	100.0% ; Pred. No. 6.4e-18;	Best Local Similarity	100.0% ; Pred. No. 5.5e-16;
Matches 28;	Conservative 0; Mismatches 0; Indels 0;	Matches 26;	Conservative 0; Mismatches 0; Indels 0;
Qy	137 VPNKVGTCVSEGSYPAGTLWHLDGKP1 164	Qy	137 VPNKVGTCVSEGSYPAGTLWHLDGK 162
Db	136 VPNKVGTCVSEGSYPAGTLWHLDGKP1 163	Db	136 VPNKVGTCVSEGSYPAGTLWHLDGK 161
RESULT 12		RESULT 13	
035444	PRELIMINARY;	AAH61182	PRELIMINARY;
ID	AAH61182;	ID	AAH61182;
AC	AC	AC	AC.
DT	01-JAN-1998 (TREMBLrel. 05 Created)	DT	14-APR-2004 (TREMBLrel. 27, Created)
DT	01-JAN-1998 (TREMBLrel. 05 Last sequence update)	DT	14-APR-2004 (TREMBLrel. 27, Last sequence update)
DT	01-OCT-2004 (TREMBLrel. 28 Last annotation update)	DT	14-APR-2004 (TREMBLrel. 27, Last annotation update)
DE	RAGE (Advanced glycosylation end product-specific receptor).	DE	Advanced Glycosylation end product-specific receptor.
GN	Name=Synonyms=Ager;	OS	Mus musculus (Mouse).
OS	Mus musculus (Mouse).	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	OX	NCBI_TaxID=10090;
OX	NCBI_TaxID=10090;	RN	SEQUENCE FROM N.A.
RN	SEQUENCE FROM N.A.	RN	SEQUENCE FROM N.A.
RP	PubMed:14655967;	RP	PubMed:12477932;
RA	Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,	RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Derge J.G.,
RA	Campbell R.D., Hood L., Jettman E., Madan A., Schuler G.D.,	RA	Klausner R.D., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,
RA	"Analysis of the gene-dense major histocompatibility complex class III	RA	Klausner R.D., Collins F.S., Schuler G.D., Shenmen C.M., Schuler G.D.,
RT	region and its comparison to mouse.";	RA	Altschul S.P., Zeeberg B., Buetow K.H., Wagner L., Schaefer C.P., Bhat N.K.,
RT	Genome Res. 13:2621-2636 (2003).	RA	Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RN	[2]	RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RP	SEQUENCE FROM N.A.	RA	Scaplecon M., Soares M.B., Bonaldo M.F., Carninci P., Scheetz T.E.,
RX	TISSUE=Lung and heart; MEDLINE:22388257; Published:12477932;	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	RA	Raha S.S., Loquelandano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA	Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,	RA	Richards J., Hale S., Garcia A.M., Malek J.A., Gunaratne P.H.,
RA	Campbell R.D., Hood L., Jettman E., Madan A., Schuler G.D.,	RA	Richardson D.K., Muzny D.M., Sodergren E.J., Hale S., Garcia A.M.,
RA	"Analysis of the gene-dense major histocompatibility complex class III	RA	Villalon D.K., Muzny D.M., Sodergren E.J., Hale S., Garcia A.M.,
RT	region and its comparison to mouse.";	RA	Fahy J., Helton B., Kettman M., Madan A., Schuler G.D.,
RT	Genome Res. 13:2621-2636 (2003).	RA	Whiting M., Madan A., Young A.C., Shevchenko A., Bouffard G.G.,
RN	[2]	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RP	SEQUENCE FROM N.A.	RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RX	TISSUE=Lung and heart; MEDLINE:22388257; Published:12477932;	RA	Krywinski M.I., Skalska U., Shaila D.E., Schein J.E., Schein U.R.,
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,	RA	Jones S.J., Marra M.A., Schuler G.D.,
RA	Xie T., Rowen L., Aguado B., Ahearn M.E., Madan A., Qin S.,	RA	"Generation and initial analysis of more than 15,000 full-length human
RA	Campbell R.D., Hood L., Jettman E., Madan A., Schuler G.D.,	RA	and mouse cDNA sequences.";
RA	"Generation and initial analysis of more than 15,000 full-length human	RT	sequences";
RA	cDNA sequences.";	RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN	[2]	RN	SEQUENCE FROM N.A.
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
RC	TISSUE=Lung and heart;	RC	TISSUE=Lung and heart;
RA	Strausberg R.;	RA	Strausberg R.;
RA	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.	RA	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.

FT DOMAIN 23 352 Extracellular (Potential).
 FT TRANSMEM 353 373 Potential.
 FT DOMAIN 374 416 Cyttoplasmic (Potential).
 FT DOMAIN 23 115 Ig-like V-type.
 FT DOMAIN 123 220 Ig-like C2-type 1.
 FT DOMAIN 238 327 Ig-like C2-type 2.
 FT DISULFID 38 98 Potential.
 FT DISULFID 143 207 Potential.
 FT DISULFID 269 311 Potential.
 FT CARBOHYD 25 25 N-Linked (GlcNAc. . .) (Potential).
 FT CARBOHYD 80 80 N-Linked (GlcNAc. . .) (Potential).
 FT DOMAIN 391 396 Poly-Glu.
 SQ SEQUENCE 416 AA; 44182 MW; B703815573E767AE CRC64;

 Query Match 5.9%; Score 24; DB 1; Length 416;
 Best Local Similarity 100.0%; Pred. No. 4.9e-14;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 237 EVOLVVEPEGGAVAPGGTVLICE 260
 Db 247 EVOLVVEPEGGAVAPGGTVLICE 270

Search completed: December 6, 2004, 15:17:45
 Job time : 195 secs

Best Local Similarity 100.0%; Pred. No. 0;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGTAGAWLVLVLSMGAIVGAQNITARIGEPLVKCKGAPKKPQRLEWKLNTRTEA 60
 Db 1 MAAGTAGAWLVLVLSMGAIVGAQNITARIGEPLVKCKGAPKKPQRLEWKLNTRTEA 60
 Qy 61 WKVLSPOGGPMDSVARVLPLNGSLFLPAVGIODEGIFRCOAMNRNGKETKSNYRVRVQI 120
 Db 61 WKVLSPOGGPMDSVARVLPLNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVRVQI 120
 Qy 121 PGKPEIVDASSELTAGYPNKVGTCVSEGYPAGTISWHLDSKPLVNEKGYSVKEQTRH 180
 Db 121 PGKPEIVDASSELTAGYPNKVGTCVSEGYPAGTISWHLDSKPLVNEKGYSVKEQTRH 180
 Qy 181 PETGLFTLQSELMVTPARGGDRPTFCSFSGPLPHRALTAPIQPWRPVPLBEVQL 240
 Db 181 PETGLFTLQSELMVTPARGGDRPTFCSFSGPLPHRALTAPIQPWRVWEPVPLBEVQL 240
 Qy 241 VVEPEGGAAVAPGSGTVLTLCEVAQSPQHWWKDGVLPLPPSPVLLPEIGPQDGOTYS 300
 Db 241 VVEPEGGAAVAPGSGTVLTLCEVAQSPQHWWKDGVLPLPPSPVLLPEIGPQDGOTYS 300
 Qy 301 CYATHSSHHGPQESRAVSVTIIIBGEGETGATSYGGSGLGTIALALGIGLGTAAALIGV 360
 Db 301 CYATHSSHHGPQESRAVSVTIIIBGEGETGATSYGGSGLGTIALALGIGLGTAAALIGV 360
 Qy 361 ILWQRQRGEREKAPENQEERERAILNOSEPEACESSTCGP 404
 Db * 361 ILWQRQRGEREKAPENQEERERAILNOSEPEACESSTCGP 404

RESULT 2
 ABP65011 standard; protein; 404 AA.
 ID ABP65011
 XX
 AC ABP65011;
 DT 25-FEB-2003 (first entry)
 XE Human Protein SEQ ID 671.
 KW Human; expressed sequence tag; EST; haematopoietic disorder;
 KW peripheral nervous system disease; viral infection;
 KW immune deficiency; immune disorder; bacterial infection; allergy; cancer;
 KW fungal infection; autoimmune disorder; coagulation disorder; nootropic;
 KW anti-allergic; anti-inflammatory; immunosuppressive; neuroprotective;
 KW cytostatic; haemostatic; virucide; antibacterial; fungicide;
 KW immunostimulant; cerebroprotective.
 XX Homo sapiens.
 OS Homo sapiens.
 PN WO200259260-A2.
 XX
 PD 01-AUG-2002.
 PP 16-NOV-2001; 2001WO-US042990.
 PR 17-NOV-2000; 2000US-00714936.
 XX
 PA (HYSEQ INC.
 PI Tang YT, Goodrich RW, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA;
 PI Ren F, Xue AJ, Yang Y, Wehrman T, Drmanac RT;
 XX
 DR WPI: 2002-590824/63.
 DR N-PSDB; ABQ99597.
 PR New isolated polynucleotide, useful in research, diagnostic or therapeutic methods, e.g. preventing or treating disorders involving aberrant protein expression or biological activity.
 PR Human receptor of advanced glycation end products (RAGE).

PS Claim 20; SEQ ID NO 671; 394PD; English.
 XX The present invention relates to novel human coding sequences (ABQ99268-
 CC ABQ9608) and proteins (ABP64682-ABP65022). The sequences are useful in
 CC therapeutic, diagnostic and research methods. The polynucleotides may be
 CC used in the field of molecular biology as hybridisation probes, primers
 CC for PCR, for chromosomal and gene mapping, for the recombinant production
 CC of protein, or in generation of anti-sense DNA or RNA. The
 CC polynucleotides are useful in diagnostics as expressed sequence tags
 CC (ESTs) for identifying expressed genes or for physical mapping of the
 CC human genome. The proteins may be used as molecular weight markers, or as
 CC nutritional sources or supplements. The proteins may be used to maintain
 CC and expand cell population in a totipotential or pluripotential state
 CC and used for re-engineering damaged or diseased tissues, transplantations. The
 CC manufacture of bio-pharmaceuticals or the development of bio-sensors. The
 CC polynucleotides and proteins are useful for preventing, treating or
 CC ameliorating disorders involving aberrant protein expression or
 CC biological activity, e.g. haematopoietic disorders, central/peripheral
 CC nervous system diseases, mechanical and traumatic disorders, non-healing
 CC wounds, immune deficiencies and disorders, infectious diseases caused by
 CC viral, bacterial or fungal infection, autoimmune disorders, allergic
 CC reactions and conditions, coagulation disorders, or cancer. The
 CC polynucleotide sequences of the invention were assembled from ESTs
 CC isolated mainly by sequencing by hybridisation, and in some cases,
 CC sequences obtained from one or more public databases. Note: The sequence
 CC data for this patent did not form part of the printed specification, but
 CC was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX Sequence 404 AA;
 SQ Query Match 100.0%; Score 404; DB 5; Length 404;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAAGTAGAWLVLVLSMGAIVGAQNITARIGEPLVKCKGAPKKPQRLEWKLNTRTEA 60
 Db 1 MAAGTAGAWLVLVLSMGAIVGAQNITARIGEPLVKCKGAPKKPQRLEWKLNTRTEA 60
 Qy 61 WKVLSPOGGPMDSVARVLPLNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVRVQI 120
 Db 61 WKVLSPOGGPMDSVARVLPLNGSLFLPAVGIODEGIFRCQAMNRNGKETKSNYRVRVQI 120
 Qy 121 PGKPEIVDASSELTAGYPNKVGTCVSEGYPAGTISWHLDSKPLVNEKGYSVKEQTRH 180
 Db 121 PGKPEIVDASSELTAGYPNKVGTCVSEGYPAGTISWHLDSKPLVNEKGYSVKEQTRH 180
 Qy 181 PETGLFTLQSELMVTPARGGDRPTFCSFSGPLPHRALTAPIQPWRVWEPVPLBEVQL 240
 Db 181 PETGLFTLQSELMVTPARGGDRPTFCSFSGPLPHRALTAPIQPWRVWEPVPLBEVQL 240
 Qy 241 VVEPEGGAAVAPGSGTVLTLCEVAQSPQHWWKDGVLPLPPSPVLLPEIGPQDGOTYS 300
 Db 241 VVEPEGGAAVAPGSGTVLTLCEVAQSPQHWWKDGVLPLPPSPVLLPEIGPQDGOTYS 300
 Qy 301 CYATHSSHHGPQESRAVSVTIIIBGEGETGATSYGGSGLGTIALALGIGLGTAAALIGV 360
 Db 301 CYATHSSHHGPQESRAVSVTIIIBGEGETGATSYGGSGLGTIALALGIGLGTAAALIGV 360
 Qy 361 ILWQRQRGEREKAPENQEERERAILNOSEPEACESSTCGP 404
 Db 361 ILWQRQRGEREKAPENQEERERAILNOSEPEACESSTCGP 404

RESULT 3
 ADF31292
 ID ADF31292 standard; protein; 404 AA.
 XX
 AC ADF31292;
 DT 12-FEB-2004 (first entry)
 XX
 DE Human receptor of advanced glycation end products (RAGE).

XX	human; receptor; advanced glycation end product; RAGE;	DE	Human receptor of advanced glycation (RAGE) protein.
KW	receptor of advanced glycation end product; high purity.	XX	
RW		KW	diabetic complication factor; receptor of advanced glycation end product;
XX		KW	RAGE binding substance adsorption ligand; water-insoluble carrier;
OS		KW	biological evaluation; diabetic complication; renal-disease; human.
Homo sapiens.		XX	
PN	JP20033306500-A.	OS	Homo sapiens.
XX	28-OCT-2003.	XX	
XX	JP20033306499-A.	PN	
PF	05-FEB-2003; 2003JP-00027992.	XX	
XX	28-OCT-2003.	PD	
PR	15-FEB-2002; 2002JP-00038380.	XX	
XX	PA (TORAY IND INC.	PF	05-FEB-2003; 2003JP-00027991.
PA		XX	15-FEB-2002; 2002JP-00038378.
XX	WPI; 2004-015267/02.	PR	
XX	Purifying receptor of advanced glycation end products derivative	PA	(TORAY) TORAY IND INC.
PT	containing Igv domain of receptor of advanced glycation end product using	XX	
PT	one or more affinity columns.	XX	
XX	DISCLOSURE; SEQ ID NO 1; 13PP; Japanese.	XX	
PS		XX	Obtaining diabetic complication factor comprises contacting biological
XX	PT	XX	fluid with adsorbent, and immobilizing receptor of advanced glycation end
CC	purifying receptor of advanced glycation end product derivative. The	XX	products binding substance ligand on carrier.
CC	method enables simple, rapid with high yield and high purity manufacture	XX	
CC	of RAGE derivative. The present sequence represents the amino acid	XX	
CC	sequence of human receptor of advanced glycation end products (RAGE).	XX	
XX	Sequence 404 AA;	XX	This invention relates to a novel method of obtaining a diabetic
SQ	1 MAAGTAVGAWVLVLSLWGAVGQAONITARIGEPLVLCKGAKPKKPQRLWEKLNTGRTEA	XX	complication factor which comprises contacting liquid from a biological
Query	60	DB	fluid with an adsorbent (RAGE) binding substance adsorption ligand on a
Db	1 MAAGTAVGAWVLVLSLWGAVGQAONITARIGEPLVLCKGAKPKKPQRLWEKLNTGRTEA	60	water-insoluble carrier, cleaning the adsorbent in an aqueous solution,
Qy	61 WKYLSPQQGGPWDSVARVLPNGSLFLPAVGIDFRCQAMNRNGKETKSNYRVRYQI	61	separating and recovering the diabetic complication factor by contracting
Db	61 WKYLSPQQGGPWDSVARVLPNGSLFLPAVGIDFRCQAMNRNGKETKSNYRVRYQI	61	the adsorbent with the aqueous solution. The method is useful for
Qy	120 WKYLSPQQGGPWDSVARVLPNGSLFLPAVGIDFRCQAMNRNGKETKSNYRVRYQI	120	carrying out biological evaluation which involves determining advanced
Db	121 PGKPEIVDVSASELTAGVNPVKGTCVSESSYPAGTLSWHLGKLPVNKGVSYKEQTRH	120	degree of diabetic complication or degree of a renal-disease.
Qy	121 PGKPEIVDVSASELTAGVNPVKGTCVSESSYPAGTLSWHLGKLPVNKGVSYKEQTRH	180	SEQ Sequence 404 AA;
Db	121 PGKPEIVDVSASELTAGVNPVKGTCVSESSYPAGTLSWHLGKLPVNKGVSYKEQTRH	180	Query Match 100.0%; Score 404; DB 8; Length 404;
Qy	180 PETGLFLQSELWVTPARGDPRTFSCSFSPGLPRHRALRTAPIQPRWEPVPLEVQL	240	Best Local Similarity 100.0%; Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;
Db	181 PETGLFLQSELWVTPARGDPRTFSCSFSPGLPRHRALRTAPIQPRWEPVPLEVQL	240	Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	240 VVEPEGGAYA PGGTIVTLLTCEVPAQSPQIHMWDGVPLPLPPSPVLLPEIGPODGOTYS	300	Qy 1 MAAGTAVGAWVLVLSLWGAVGQAONITARIGEPLVLCKGAKPKKPQRLWEKLNTGRTEA 60
Db	240 VVEPEGGAYA PGGTIVTLLTCEVPAQSPQIHMWDGVPLPLPPSPVLLPEIGPODGOTYS	300	Db 1 MAAGTAVGAWVLVLSLWGAVGQAONITARIGEPLVLCKGAKPKKPQRLWEKLNTGRTEA 60
Qy	300 VVEPEGGAYA PGGTIVTLLTCEVPAQSPQIHMWDGVPLPLPPSPVLLPEIGPODGOTYS	300	Qy 61 WKYLSPQQGGPWDSVARVLPNGSLFLPAVGIDFRCQAMNRNGKETKSNYRVRYQI
Db	300 VVEPEGGAYA PGGTIVTLLTCEVPAQSPQIHMWDGVPLPLPPSPVLLPEIGPODGOTYS	300	Db 61 WKYLSPQQGGPWDSVARVLPNGSLFLPAVGIDFRCQAMNRNGKETKSNYRVRYQI
Qy	360 ILMQRQRGEERKAPEQEEERBAAEINQSEEPEAGESTGGP 404	360	Qy 121 PGKPEIVDVSASELTAGVNPVKGTCVSESSYPAGTLSWHLGKLPVNKGVSYKEQTRH 180
Db	360 ILMQRQRGEERKAPEQEEERBAAEINQSEEPEAGESTGGP 404	360	Db 121 PGKPEIVDVSASELTAGVNPVKGTCVSESSYPAGTLSWHLGKLPVNKGVSYKEQTRH 180
Qy	361 CVATHSSHGPQESRAVSIIEPEEGPTAGSVCGSGLGTLALALGILGLGTAALLIGV	360	Qy 181 PETGLFLQSELWVTPARGDPRTFSCSFSPGLPRHRALRTAPIQPRWEPVPLEVQL
Db	361 CVATHSSHGPQESRAVSIIEPEEGPTAGSVCGSGLGTLALALGILGLGTAALLIGV	360	Db 181 PETGLFLQSELWVTPARGDPRTFSCSFSPGLPRHRALRTAPIQPRWEPVPLEVQL
Qy	361 CVATHSSHGPQESRAVSIIEPEEGPTAGSVCGSGLGTLALALGILGLGTAALLIGV	360	Qy 241 VVEPEGGAYA PGGTIVTLLTCEVPAQSPQIHMWDGVPLPLPPSPVLLPEIGPODGOTYS
Db	361 CVATHSSHGPQESRAVSIIEPEEGPTAGSVCGSGLGTLALALGILGLGTAALLIGV	360	Db 241 VVEPEGGAYA PGGTIVTLLTCEVPAQSPQIHMWDGVPLPLPPSPVLLPEIGPODGOTYS
Qy	361 CVATHSSHGPQESRAVSIIEPEEGPTAGSVCGSGLGTLALALGILGLGTAALLIGV	360	Qy 301 CVATHSSHGPQESRAVSIIEPEEGPTAGSVCGSGLGTLALALGILGLGTAALLIGV
Db	361 CVATHSSHGPQESRAVSIIEPEEGPTAGSVCGSGLGTLALALGILGLGTAALLIGV	360	Db 301 CVATHSSHGPQESRAVSIIEPEEGPTAGSVCGSGLGTLALALGILGLGTAALLIGV
Qy	361 CVATHSSHGPQESRAVSIIEPEEGPTAGSVCGSGLGTLALALGILGLGTAALLIGV	360	Qy 361 ILMQRQRGEERKAPEQEEERBAAEINQSEEPEAGESTGGP 404
Db	361 ILMQRQRGEERKAPEQEEERBAAEINQSEEPEAGESTGGP 404	360	Db 361 ILMQRQRGEERKAPEQEEERBAAEINQSEEPEAGESTGGP 404

RESULT 5

RESULT 4
 ADF42983
 ID ADF42983 standard; Protein: 404 AA.
 XX
 AC
 DT 12-FEB-2004 (first entry)

ADK00129 ID ADK00129 standard; protein; 404 AA. XX AC ADK00129; XX DT 20-MAY-2004 (first entry) XX DE Human RAGE protein. XX KW Advanced Glycation End Product Ligand Binding Element; RAGE-LBE; KW Cytostatic; Antidiabetic; Nootropic; Antiarthritic; Osteopathic; KW Neuroprotective; Antinflammatory; Dermatological; Immunosuppressive; KW Vasotrophic; Antipsoriatic; Antibacterial; Antiarteriosclerotic; KW Amyloidosis; cancer; Crohn's disease; diabetes; Alzheimer's disease; KW Chronic inflammation; osteoarthritis; irritable bowel disease; KW Multiple sclerosis; psoriasis. XX OS Homo sapiens. OS Synthetic. PN WO2004016229-A2. XX PD 26-FEB-2004. XX PF 18-AUG-2003; 2003WO-US025996. XX PR 16-AUG-2002; 2002US-0404205P. XX PA (AMPH) WYETH. XX Pittman DD, Clancy B, Larsen G, Trepicchio WL, Brennan FM; PI Feldmann M, Foxwell BJM, Feldman JI; XX WPI: 2004-192067/18. DR N-PSD8; ADK0130. XX PT New fusion protein comprising a Receptor for Advanced Glycation End PT Product Ligand Binding Element (RAGE-LBE) and an immunoglobulin element, PT useful for preparing a composition for treating e.g., Alzheimer's PT disease. XX PS Disclosure; SEQ ID NO 43; 100pp; English. XX CC The present invention relates to a new fusion protein comprises a (RAGE- CC LBE) and an immunoglobulin element. The fusion protein is useful for CC preparing a composition for treating RAGE-associated disorder such as CC amyloidosis, cancer, Crohn's disease, diabetes, complications of CC diabetes, prion-related disorders, vasculitis, nephropathies, CC retinopathies and/or neuropathies; Alzheimer's disease, chronic CC inflammatory disease e.g., rheumatoid arthritis, osteoarthritis, CC irritable bowel disease, multiple sclerosis, psoriasis or lupus, acute CC inflammatory disease e.g., sepsis, or cardiovascular disease, e.g., CC atherosclerosis or restenosis. The present sequence represents human RAGE CC protein. XX SQ Sequence 404 AA;	Qy 1 MAAGTAVCAWNLVLSLNGAVVGAQNTARIGSPVPLVKKGAKPKPPORLEWKLNTRTEA 60 Db 1 MAAGTAVCAWNLVLSLNGAVVGAQNTARIGSPVPLVKKGAKPKPPORLEWKLNTRTEA 60 Qy 61 WKVLSPOGGGPWDSSVARVLPNGSLFLPAGVQDGEGIKRQANTRNGKTSKNYRVYQI 120 Db 61 WKVLSPOGGGPWDSSVARVLPNGSLFLPAGVQDGEGIKRQANTRNGKTSKNYRVYQI 120 Qy 121 PGKPEIVDSASELTAGVNPVKGTCVSEGSYPACTLSWLDGKPLVNPNEGVSKVEOTRH 180 Db 121 PGKPEIVDSASELTAGVNPVKGTCVSEGSYPACTLSWLDGKPLVNPNEGVSKVEOTRH 180 Qy 121 PGKPEIVDSASELTAGVNPVKGTCVSEGSYPACTLSWLDGKPLVNPNEGVSKVEOTRH 180 Db 121 PGKPEIVDSASELTAGVNPVKGTCVSEGSYPACTLSWLDGKPLVNPNEGVSKVEOTRH 180	Query Match 100.0%; Score 404; DB 8; Length 404; Best Local Similarity 100.0%; Pred. No. 0; Matches 404; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match 99.8%; Score 403; DB 5; Length 404; Best Local Similarity 100.0%; Pred. No. 0; Matches 403; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2 AAGTAGAWVILVLSLKGAVVGAONITARIGEPLVLCKGAKPKKPQRLEWKUNTRTEAW 61
 Db 2 RAASTGVAWVILVLSLKGAVVGAONITARIGEPLVLCKGAKPKKPQRLEWKUNTRTEAW 61
 QY 62 KVLSQPGGGPMDSVARVLPNGSLFLPAVGIDQEGIIFRCQAMNRNGKETKSNSYRVRYOIP 121
 Db 62 KVLSQPGGGPMDSVARVLPNGSLFLPAVGIDQEGIIFRCQAMNRNGKETKSNSYRVRYOIP 121
 QY 122 GKEPIVDSASELTAGPVNKVGTCVSEGSYPAGLSMLDGPBVPNEKGSKKEQTBRHP 181
 Db 122 GKEPIVDSASELTAGPVNKVGTCVSEGSYPAGLSMLDGPBVPNEKGSKKEQTBRHP 181
 Qy 182 EIGFLTLOSSLEMVTPARGSDPRPTFSCSFSPGLPRHRLAATIQLPRTWEPVPLEEVQLV 241
 Db 182 EIGFLTLOSSLEMVTPARGSDPRPTFSCSFSPGLPRHRLAATIQLPRTWEPVPLEEVQLV 241
 Qy 242 VEPGGAVAPGGTVTILCEVPAQPSPOIHMWDGYVPLPLPPSPVLLPEIGPQDGTYSC 301
 Db 242 VEPGGAVAPGGTVTILCEVPAQPSPOIHMWDGYVPLPLPPSPVLLPEIGPQDGTYSC 301
 Qy 302 VATHSSHGPOESPAVSIISIIEPGEEGPTAGSVGSGLCTLAALIGLGGCTAALLIGV 361
 Db 302 VATHSSHGPOESPAVSIISIIEPGEEGPTAGSVGSGLCTLAALIGLGGCTAALLIGV 361
 Qy 362 LMQRQRGERERKAPENOEEERERAELNQSSEPAGEGSTGGP 404
 Db 362 LMQRQRGERERKAPENOEEERERAELNQSSEPAGEGSTGGP 404

RESULT 7
ID ADE95564 standard; protein; 402 AA.

XX AC ADE95564;
 XX DT 12-FEB-2004 (first entry)
 XX DE Human NOVX16c protein.

XX NOVX protein; biochemical stimulation; physiological stimulation;
 XX cardiotonic; antiarteriosclerotic; hypotensive; cytostatic; anorectic;
 XX antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;
 XX immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
 XX nootropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;
 XX antidepressant; antiallergic; gene therapy; vaccine;
 XX NOVX-associated disorder; cardiomopathy; atherosclerosis; hypertension;
 XX cancer; obesity; skin disorder; arthritis; diabetes; glomerulonephritis;
 XX psoriasis; asthma; Parkinson's disease; asthma; schizophrenia;
 XX Alzheimer's disease; fertility disorder; NOVX16c.

XX Homo sapiens.
 XX PN WO2003050245-A2.
 XX PD 19-JUN-2003.

PF 03-DEC-2002; 2002WO-US038594.
 XX 05-DEC-2001; 2001US-0336600P.
 PR 07-DEC-2001; 2001US-0338285P.
 PR 12-DEC-2001; 2001US-0341346P.
 PR 17-DEC-2001; 2001US-0341477P.
 PR 17-DEC-2001; 2001US-0341540P.
 PR 20-DEC-2001; 2001US-0342592P.
 PR 27-DEC-2001; 2001US-0344297P.
 PR 31-DEC-2001; 2001US-034403P.
 PR 2002APR-2002; 2002US-0373288P.
 PR 15-MAY-2002; 2002US-0360981P.
 PR 11-MAY-2002; 2002US-0361495P.
 PR 28-MAY-2002; 2002US-0363534P.
 PR 28-MAY-2002; 2002US-0363744P.
 PR 29-MAY-2002; 2002US-0363829P.

PR 29-MAY-2002; 2002US-0384024P.
 PR 07-AUG-2002; 2002US-040178P.
 PR 26-AUG-2002; 2002US-040635P.
 PR 31-OCT-2002; 2002US-0040178P.
 PR 02-DEC-2002; 2002US-0040653.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chilakaturu RA,
 PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X,
 PI Jeffers ME, Ji W, Li L, Malvankar UM, Miller CE, Murphy R,
 PI Paturajan M, Payman JA, Pastelli L, Rieger DK, Shenoy SG,
 PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
 XX
 PI Alsbrook JP, Anderson DW, Boldog FL, Burgess CE, Chilakaturu RA,
 PI Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X,
 PI Jeffers ME, Ji W, Li L, Malvankar UM, Miller CE, Murphy R,
 PI Paturajan M, Payman JA, Pastelli L, Rieger DK, Shenoy SG,
 PI Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
 XX
 DR WPI; 2003-513974/4.
 DR N-PSDB; ADE95563.
 XX
 PT New NOVX polypeptides and nucleic acids, useful for preventing or
 PT treating NOVX-associated disorders, e.g. cancer, cardiomopathy,
 PT atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
 PT pharmacogenomics.
 XX
 CC Claim 2; SEQ ID NO 96; 211pp; English.
 XX
 CC This invention relates to novel NOVX proteins, and the DNA sequence which
 CC encode them, having properties related to stimulation of biochemical or
 CC physiological responses in a cell, a tissue, an organ or an organism.
 CC Compounds which modulate the proteins of the invention may have cardiotonic,
 CC antiarrheotic, antihypertensive, cytostatic, anorectic, antirheumatic,
 CC antiarthritic, antidiabetic, nephrotropic, dermatological,
 CC immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
 CC nootropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
 CC antidepressant, antiallergic or gynaecological activities. The DNA
 CC sequences of the invention may be useful for gene therapy whilst the
 CC protein sequences may allow the development of a vaccine. The protein is
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease. The invention may be useful in
 CC diagnosing, treating or preventing NOVX-associated disorders, for example
 CC cardiomopathy, atherosclerosis, hypertension, cancer, obesity,
 CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
 CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
 CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
 CC fertility disorders. The nucleic acids may further be used as
 CC hybridisation probes, in chromosome mapping, tissue typing, preventive
 CC medicine, and pharmacogenomics. The present sequence is the amino acid
 CC sequence of the human NOVX16c protein of the invention.
 XX
 SQ Sequence 402 AA;

Query Match 99.5%; Score 402; DB 7; Length 402;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MAAGTAGAWVILVLSLKGAVVGAONITARIGEPLVLCKGAKPKKPQRLEWKUNTRTEAW 60
 Db 1 MAAGTAGAWVILVLSLKGAVVGAONITARIGEPLVLCKGAKPKKPQRLEWKUNTRTEAW 60
 Qy 61 WKVLSQQGGPMDSVARVLPNGSLFLPAVGIDQEGIIFRCQAMNRNGKETKSNSYRVRYQI 120
 Db 61 WKVLSQQGGPMDSVARVLPNGSLFLPAVGIDQEGIIFRCQAMNRNGKETKSNSYRVRYQI 120
 Qy 121 PGKPEIIVDSASELTAGPNKVGTCSSESSYPACTLSHLDGKPLVNPHEKGVSYKEQTRRH 180
 Db 121 PGKPEIIVDSASELTAGPNKVGTCSSESSYPACTLSHLDGKPLVNPHEKGVSYKEQTRRH 180
 Qy 181 PETGLFTLOSELMVTPARGGDPRTFSCSFSPGLPRHRLRTAPIQPRVMEPVPLEVQL 240
 Db 181 PETGLFTLOSELMVTPARGGDPRTFSCSFSPGLPRHRLRTAPIQPRVMEPVPLEVQL 240
 Qy 181 PETGLFTQSELMTVTPARGGDPRTFSCSFSPGLPRHRLRTAPIQPRVMEPVPLEVQL 240
 Db 181 PETGLFTQSELMTVTPARGGDPRTFSCSFSPGLPRHRLRTAPIQPRVMEPVPLEVQL 240
 Qy 241 VVEPEGAVAPGGTVTLCEVAPQSPQIHMKDGVPPLPPSPVLIPEIGPQDQGTYI 300
 Db 241 VVEPEGAVAPGGTVTLCEVAPQSPQIHMKDGVPPLPPSPVLIPEIGPQDQGTYI 300
 Qy 241 VVEPEGAVAPGGTVTLCEVAPQSPQIHMKDGVPPLPPSPVLIPEIGPQDQGTYI 300
 Db 241 VVEPEGAVAPGGTVTLCEVAPQSPQIHMKDGVPPLPPSPVLIPEIGPQDQGTYI 300

Qy 301 CYATHSSHGPOESRAVSIISIEPGEEGFTAGSYGGSGLGTIALALGIGGLGTAALLIGV 360
 Db 301 CYATHSSHGPOESRAVSIISIEPGEEGFTAGSYGGSGLGTIALALGIGGLGTAALLIGV 360

Qy 361 ILMQRQRGEREERKAPENQEEERERAELNQSEPEAGGSSTG 402
 Db 361 ILMQRQRGEREERKAPENQEEERERAELNQSEPEAGGSSTG 402

RESULT 8
 ADP19666 standard; protein: 391 AA.
 XX
 AC ADP19666;
 XX
 DT 12-AUG-2004 (First entry)
 XX
 Human LP2005 protein SEQ ID NO:12.
 XX
 human; LP2005; antidiabetic; antiarthritic; nootropic; neuroprotective; nontropic; antiinflammatory; antidiabetic; antirheumatic; antiarthritic; nootropic; cytostatic; immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes; Alzheimer's disease; inflammation; rheumtoid arthritis; wound; autoimmune disease; multiple sclerosis; cancer; lupus nephritis; systemic lupus erythematosus.

OS Homo sapiens.

XX Key Location/Qualifiers

PR 1; .23

FT /label= signal

PT 24; .391

FT /label= Lp2005

XX WO200404126-A2.

XX PD 27-MAY-2004.

XX PP 05-NOV-2003; 2003WO-US032734.

XX PR 14-NOV-2002; 2002US-0426253P.

XX PA (ELIL) LILLY & CO ELI.

XX PI Na S, Perkins DR;

XX DR; 2004-411705/38.

XX N-PSDB; ADP19665.

XX New nucleic acid molecules and encoded LP polypeptides (e.g., LP2001 or LP2003) for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome identification.

XX Claim 9; SEQ ID NO 12; 111pp; English.

The present sequence represents human LP2005, which is used in the exemplification of the present invention. The present invention describes: (1) an isolated nucleic acid (1) comprising DNA having at least 95% sequence identity to a polynucleotide selected from the group consisting of: (a) a polynucleotide having a nucleotide sequence as shown in SEQ ID NO:3; (b) a polynucleotide encoding a polypeptide or mature form of a polypeptide having the amino acid sequence as shown in SEQ ID NO:1; (c) a polynucleotide fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide having a nucleotide sequence which is complementary to the nucleotide sequence of a polynucleotide as in (a), (b) or (c); (2) a vector comprising (1); (3) a host cell comprising the vector; (4) producing an LP polypeptide; (5) an isolated polypeptide produced by the above method and comprising an amino acid sequence comprising about 95% sequence identity to a sequence of amino acid residues comprising LP2001, LP2003, LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric molecule comprising an LP polypeptide fused to a heterologous amino acid

CC sequence; (7) an antibody which specifically binds to an LP polypeptide described above; (8) a composition (C) comprising an therapeutic amount of an active agent selected from an LP polypeptide, an agonist to an LP polypeptide, an antagonist to an LP polypeptide, an LP polypeptide, an anti-LP polypeptide, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a polynucleotide in combination with a pharmaceutical carrier; and (9) diagnosing or treating a mammal suffering from disease, condition or disorder associated with aberrant levels of an LP polypeptide. (C) has antidiabetic, neuroprotective, nontropic, antiinflammatory, CC antirheumatic, antiarthritic, pulmonary, cytostatic, immunosuppressive, nephrotropic and dermatological activities, and can be used in gene therapy. The compositions (C) and methods are useful for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, such as diabetes and its complications, Alzheimer's disease, CC inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple CC sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They may also be used for chromosome identification. The LP polypeptide can also be used in manufacturing a medicament for the treatment of the above -mentioned diseases, conditions or disorders associated with aberrant CC levels of the LP polypeptide.

XX

SQ Sequence 391 AA;

Query	Match	Score	Length
Best Local Similarity	92.3%	373	DB 8;
Matches	100.0%	Pred. No. 0;	Mismatches 0;
		Indels 0;	Gaps 0;

Qy 1 MAAAGTAGAWIVLVLSLWGAIVGAQNTARTIGPLVTKCKGAKPKPPORLEWKLTGRTEA 60
 Db 1 MAAGTAGAWIVLVLSLWGAIVGAQNTARTIGPLVTKCKGAKPKPPORLEWKLTGRTEA 60

Qy 61 WKVULSPQQGGPMDSAVAVLPNGSLFLPAVGQDQEGLFRCQAMNRKGKETKSMDMYRVRVYQI 120
 Db 61 WKVULSPQQGGPMDSAVAVLPNGSLFLPAVGQDQEGLFRCQAMNRKGKETKSMDMYRVRVYQI 120

Qy 121 PGKPEIVDASAEITAGYPNKVSTCVSEGSSYPATGTLSMHLDGPVLPNEKGVSVKEQTRH 180
 Db 121 PGKPEIVDASAEITAGYPNKVSTCVSEGSSYPATGTLSMHLDGPVLPNEKGVSVKEQTRH 180

Qy 181 PETGLFTLQSEIMNPARGGDPRTFCSFSGLPRIRALRTAPIPRVWEVPLEEVQL 240
 Db 181 PETGLFTLQSEIMNPARGGDPRTFCSFSGLPRIRALRTAPIPRVWEVPLEEVQL 240

Qy 241 VVEPEGAAVAPGTTAVLTCVEPAQPSQIHHNMKDGVPLPLPBSPLVLLPEIGPQDGQTS 300
 Db 241 VVEPEGAAVAPGTTAVLTCVEPAQPSQIHHNMKDGVPLPLPBSPLVLLPEIGPQDGQTS 300

Qy 301 CVATHSSHGQPSRSAVSISIEPGEEGPTASVGSSGLGTIALALGIGGLGTAALLIGV 360
 Db 301 CVATHSSHGQPSRSAVSISIEPGEEGPTASVGSSGLGTIALALGIGGLGTAALLIGV 360

Qy 361 IIWQRORRGEER 373
 Db 361 IIWQRORRGEER 373

RESULT 9
 AAW44199
 ID AAW44199 standard; protein: 340 AA.
 XX
 AC AAW44199;
 XX
 DT 14-MAY-1998 (first entry)
 XX Human soluble receptor to an advanced glycosylation end product.
 XX DE Human soluble receptor
 XX AC
 XX DT 14-MAY-1998 (first entry)
 XX Human soluble receptor
 XX Human; soluble receptor; advanced glycosylation end product; RAGE; AGE;
 XX antibody; vascular permeability; diabetes mellitus.
 XX OS Homo sapiens.
 XX PN WO9739125-A1.
 XX XX

PD	23-OCT-1997.	KW Advanced glycosylation end-product receptor; RAGE; screening; AGE;
XX	11-APR-1997;	KW vascular permeability; diabetes mellitus; treatment; atherosclerosis;
PF	97WO-EP001834.	KW Alzheimer's disease.
XX	16-APR-1996;	XX
PR	96US-00633148.	OS Homo sapiens .
XX	(SCHD) SCHERRING PATENTE AG.	XX
PA		PN WO9739121-A1.
XX		XX
PI	Morser MJ, Nagashima M, Hollander DA,	PD 23-OCT-1997.
XX	WPI: 1997-558580/51.	XX
DR	DR 11-APR-1997;	97WO-EP001832.
N-PSDB;	AAV12394.	XX
XX	16-APR-1996;	96US-00633147.
PT	Anti-advanced glycosylation end product polypeptide antibody - prevents receptor binding and therefore reduces vascular permeability, useful to treat diabetes mellitus.	XX
PT	Claim 2 ; Page 40-41; 90pp; English.	XX
PS		PI Morser MJ, Nagashima M;
XX	DR WPI: 1997-526458/48.	XX
CC	The present sequence represents a soluble human receptor to an advanced glycosylation end product (RAGE) polypeptide. The present invention describes an isolated antibody (Ab), specifically immunoreactive with RAGE. Advanced glycosylation end products (AGE) of proteins are non-enzymatically glycosylated proteins, which accumulate in vascular tissue in ageing, and at an accelerated rate in individuals with diabetes. The Ab, which prevents the interaction between an AGE and it's receptor (RAGE), reduces vascular permeability. The Ab can be used to treat diabetes mellitus symptoms, e.g. microvasculopathy, occlusive vascular disorders, neuropathy, retinopathy, nephropathy, haemodialysis associated amyloidosis or atherosclerosis. The Ab can also be used for the isolation and purification of human RAGE polypeptide.	XX
CC	Sequence 340 AA;	XX
CC	Query Match 84.2%; Score 340; DB 2; Length 340; Best Local Similarity 100.0%; Pred. No. 2.4e-300; Matches 340; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	XX
Qy	1 MAAGTAGAWLVLISLWGAIVGAGNITARIIGRPLVLKCKGAKPKPPQRLWEKLNTGRTEA 60	Qy 1 MAAGTAGAWLVLISLWGAIVGAGNITARIIGRPLVLKCKGAKPKPPQRLWEKLNTGRTEA 60
Db	1 MAAGTAGAWLVLISLWGAIVGAGNITARIIGRPLVLKCKGAKPKPPQRLWEKLNTGRTEA 60	Db 1 MAAGTAGAWLVLISLWGAIVGAGNITARIIGRPLVLKCKGAKPKPPQRLWEKLNTGRTEA 60
Qy	61 WKVLSPOGGPMDSVARYVLPNGSLFLPAGVQDDEGIFRQAMNRNGKETKSNYRVRYQI 120	Qy 61 WKVLSPOGGPMDSVARYVLPNGSLFLPAGVQDDEGIFRQAMNRNGKETKSNYRVRYQI 120
Db	61 WKVLSPOGGPMDSVARYVLPNGSLFLPAGVQDDEGIFRQAMNRNGKETKSNYRVRYQI 120	Db 61 WKVLSPOGGPMDSVARYVLPNGSLFLPAGVQDDEGIFRQAMNRNGKETKSNYRVRYQI 120
Qy	121 PGKEPIVDASSELTAGVNPKVGTCVSEGSYPAGTLSWILDGKPLVPNEKGVSYKEQTRH 180	Qy 121 PGKEPIVDASSELTAGVNPKVGTCVSEGSYPAGTLSWILDGKPLVPNEKGVSYKEQTRH 180
Db	121 PGKEPIVDASSELTAGVNPKVGTCVSEGSYPAGTLSWILDGKPLVPNEKGVSYKEQTRH 180	Db 121 PGKEPIVDASSELTAGVNPKVGTCVSEGSYPAGTLSWILDGKPLVPNEKGVSYKEQTRH 180
Qy	181 PETGLFTLQSELMVTPARGGDPPTEFCSFSPGILPRHARLTAPIQPVWEPYPLEEVQL 240	Qy 181 PETGLFTLQSELMVTPARGGDPPTEFCSFSPGILPRHARLTAPIQPVWEPYPLEEVQL 240
Db	181 PETGLFTLQSELMVTPARGGDPPTEFCSFSPGILPRHARLTAPIQPVWEPYPLEEVQL 240	Db 181 PETGLFTLQSELMVTPARGGDPPTEFCSFSPGILPRHARLTAPIQPVWEPYPLEEVQL 240
Qy	241 VVEPEGGAVA PGGTVLTLTCEVPAQSPQTHMMDGVPLPLPPSPVLLPEIGQDQGTYS 300	Qy 241 VVEPEGGAVA PGGTVLTLTCEVPAQSPQTHMMDGVPLPLPPSPVLLPEIGQDQGTYS 300
Db	241 VVEPEGGAVA PGGTVLTLTCEVPAQSPQTHMMDGVPLPLPPSPVLLPEIGQDQGTYS 300	Db 241 VVEPEGGAVA PGGTVLTLTCEVPAQSPQTHMMDGVPLPLPPSPVLLPEIGQDQGTYS 300
Qy	301 CVATHSSHGPQESRAVSIISIEPQESEGPTAGSVEGSGLGT 340	Qy 301 CVATHSSHGPQESRAVSIISIEPQESEGPTAGSVEGSGLGT 340
Db	301 CVATHSSHGPQESRAVSIISIEPQESEGPTAGSVEGSGLGT 340	Db 301 CVATHSSHGPQESRAVSIISIEPQESEGPTAGSVEGSGLGT 340
RESULT 10		Qy 181 PETGLFTLQSELMVTPARGGDPPTEFCSFSPGILPRHARLTAPIQPVWEPYPLEEVQL 240
AAW33753		Db 181 PETGLFTLQSELMVTPARGGDPPTEFCSFSPGILPRHARLTAPIQPVWEPYPLEEVQL 240
ID	AAW33753 standard; protein; 340 AA.	XX
XX	08-MAY-1998 (first entry)	XX
DT	Human RAGE polypeptide (340 amino acid residues).	XX
DX		XX
XX		XX

Qy	301	CVATHSSHGPOESRAYSISIISIIPGGERGPATAGSGVGSSGLGT	340	
Db	301	CVATHSSHGPOESRAYSISIISIIPGGERGPATAGSGVGSSGLGT	340	
		RESULT 11		
AAM46746	ID	AAM46746 standard; protein; 339 AA.		
	XX	AAM46746;		
	XX	DT-APR-2002 (first entry)		
	XX	Human sRAGE protein SEQ ID NO 2.		
	XX	KW Human; RAGE; receptor for advanced glycated endproduct; receptor; antidiabetic; neuroprotective; cytostatic; antiinflammatory; vasotrophic; nephrotropic; dermatological; antiarteriosclerotic; nototropic; diabetes; Alzheimer's disease; cancer; inflammation; kidney failure; systemic lupus; nephritis; erectile dysfunction; atherosclerosis.		
	XX	OS Homo sapiens.		
	XX	PN WC200192892-A2.		
	PD	06-DBC-2001.		
	XX	PR 30-MAY-2001; 2001WO-US017447.		
	XX	PR 30-MAY-2000; 2000US-0207342P.		
	XX	PR 05-MAR-2001; 2001US-00799152.		
	XX	(TRAN-) TRANS TECH PHARMA.		
	PA	Shahbaz M;		
	XX	WPI; 2002-114372/15.		
	PS	Detecting a receptor for advanced glycated endproducts (RAGE) modulators, for treating e.g., cancer, diabetes or inflammation, comprises measuring the amount of bound anti-RAGE antibody.		
	XX	Claim 2; Fig 2; 49pp; English.		
	CC	The invention relates to detecting receptor for advanced glycated endproducts (RAGE) modulators comprising determining the amount of RAGE protein or its fragment bound to the pre-adsorbed ligand by measuring the amount of anti-RAGE antibody bound to the solid surface. The method is useful for rapid, high-throughput identification of compounds that modulate RAGE. The compounds are useful for treating symptoms of diabetes disease, cancer, inflammatory late complications, amyloidosis, Alzheimer's disease, lupus nephritis, systemic lupus nephritis or kidney failure, systemic lupus nephritis, erectile dysfunction and atherosclerosis		
	CC	Sequence 339 AA;		
	CC	Query Match 83.7%; Score 338; DB 5; Length 339; Best Local Similarity 100.0%; Pred. No. 1.5e-298; Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
	CC	2 AAGTAGAAGWLVLSINGCAVGAQNTIPARIGPLVKCKGAKPKPPORLKLNTGRTEAW 61		
	CC	2 AAGTAGAAGWLVLSINGCAVGAQNTIPARIGPLVKCKGAKPKPPORLKLNTGRTEAW 61		
	CC	62 KVLSPQQGPMDSVARYL PNSGLFLPAGIDEGIFRCQAMNRNGKETSKNYRVYQIP 121		
	CC	62 KVLSPQQGPMDSVARYL PNSGLFLPAGIDEGIFRCQAMNRNGKETSKNYRVYQIP 121		
	CC	122 GKPEIVDVSASELTAGVNKVGTCTCGSYPAGTSLWHDCKPLVNEKGYSVKEQTTRHP 181		
	CC	122 GKPEIVDVSASELTAGVNKVGTCTCGSYPAGTSLWHDCKPLVNEKGYSVKEQTTRHP 181		
	SQ	Query Match 83.7%; Score 338; DB 5; Length 339; Best Local Similarity 100.0%; Pred. No. 1.5e-298; Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
	DB	RESULT 12		
	DB	ABB82164 standard; protein; 339 AA.		
	DB	ID ABB82164 standard; protein; 339 AA.		
	XX	XX AC ABB82164;		
	XX	XX DT 23-DEC-2002 (first entry)		
	XX	XX DE Human soluble RAGE (sRAGE).		
	XX	XX XX Receptor for Advanced Glycated end product; RAGE; recombinant; rootropic; antarteriosclerotic; antidiabetic; cyostatic; nephrotropic; vasotropic; neuroprotective; antiinflammatory; gene therapy; human.		
	XX	XX OS Homo sapiens.		
	XX	XX PN WO200270667-A2.		
	XX	XX PD 12-SEP-2002.		
	XX	XX PF 05-MAR-2002; 2002WO-US006881.		
	XX	XX PR 05-MAR-2001; 2001US-0273418P.		
	XX	XX PA (TRAN-) TRANSTECH PHARMA INC.		
	XX	XX PI Harris R, Shen J, Shahbaz M;		
	XX	XX DR WPI; 2002-71343/77.		
	XX	XX DR N-PSDB; ABQ79956.		
	XX	XX High level expression of recombinant Receptors for Advanced Glycated end products (RAGE) Proteins for treating increased levels of advanced glycosylation end products, comprises infecting cells with a high titer recombinant virus.		
	XX	XX Example; Fig 2B; 51pp; English.		
	XX	XX The invention relates to a method for high level expression of recombinant forms of the Receptor for Advanced Glycated end products (RAGE) or its fragments. The method involves (i) subcloning a nucleotide sequence encoding RAGE or its fragment into a virus; (ii) preparing a high titer stock of recombinant virus; and (iii) infecting host cells with the high titer recombinant virus under conditions such that CC predetermined levels of RAGE or its fragment is produced, where the CC predetermined levels of RAGE comprises at least 25 mg recombinant protein CC per liter of culture. The method is useful for high level expression of recombinant RAGE polypeptide or its fragment which may be useful in preventing, treating or ameliorating diseases associated with increased CC levels of advanced glycosylation end products, such as atherosclerosis, CC diabetes and its symptoms, amyloidosis, kidney failure, Alzheimer's CC disease, inflammation, systemic lupus nephritis, inflammatory lupus CC nephritis, cancer or erectile dysfunction. The present sequence CC represents the amino acid sequence of human sRAGE (soluble, extracellular CC portion of RAGE)		
	SQ	Sequence 339 AA;		
	SQ	Query Match 83.7%; Score 338; DB 5; Length 339; Best Local Similarity 100.0%; Pred. No. 1.5e-298; Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
	DB	Query Match 83.7%; Score 338; DB 5; Length 339; Best Local Similarity 100.0%; Pred. No. 1.5e-298; Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		

Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MAAGTAGAWLVLISLNGAVQGNITARIGELVLKCKGAKPKPPORLEWKLNTRGTEA 60
 Db 1 MAAGTAGAWLVLISLNGAVQGNITARIGELVLKCKGAKPKPPORLEWKLNTRGTEA 60
 PR 26-AUG-2002; 2002US-0406353P.
 PR 31-OCT-2002; 2002US-00401788.
 PR 02-DEC-2002; 2002US-00406553.
 XX
 XX (CURA-) CURAGEN CORP.

Qy 61 WKLSPQQGGPMDSVARYLVLPGNSLFLPAVGIDQEGIFRCQAMNRNGKETGSNFRVRYQI 120
 Db 61 WKLSPQQGGPMDSVARYLVLPGNSLFLPAVGIDQEGIFRCQAMNRNGKETGSNFRVRYQI 120
 PR Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chillakuru RA;
 PR Bainger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo X;
 PR Jeffers MB, Ji W, Li L, Malvankar UM, Miller CE, Murphrey R;
 PR Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shetey SG;
 PR Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;
 PR WPI; 2003-513974/48.
 XX
 DR N-PSDBB; ADE95565.

Qy 121 PGKPEIVDSASELTAGVNKGTVSESSYGPAGLVPNEKGTVSEKTRRH 180
 Db 121 PGKPEIVDSASELTAGVNKGTVSESSYGPAGLVPNEKGTVSEKTRRH 180
 PR New NOXV polypeptides and nucleic acids, useful for preventing or
 PR treating NOX-associated disorders, e.g. cancer, cardiomyopathy,
 PR atherosclerosis or diabetes, and in chromosome mapping, tissue typing or
 PR pharmacogenomics.
 XX
 PS Claim 2; SEQ ID NO 98; 211pp; English.
 XX
 This invention relates to novel NOX proteins, and the DNA sequence which
 encode them, having properties related to stimulation of biochemical or
 physiological responses in cell, a tissue, an organ or an organism.
 Compounds which modulate the proteins of the invention may have cardiotonic,
 antiarrhythmic, hypotensive, cytostatic, anorectic, antirheumatic,
 antiarthritic, antidiabetic, nephrotropic, dermatological,
 immunosuppressive, anti-HIV, antiinflammatory, neuroprotective,
 nootropic, antipsoriatic, antiparkinsonian, antiasthmatic, neuroleptic,
 antidepressant, antiallergic, gynaecological activities. The DNA
 sequences of the invention may be useful for gene therapy whilst the protein is
 useful in the manufacture of a medicament for treating a syndrome
 associated with a human disease. The invention may be useful in
 diagnosing, treating or preventing NOX-associated disorders, for example
 CC cardiomopathy, atherosclerosis, hypertension, cancer, obesity,
 CC rheumatoid arthritis, diabetes, glomerulonephritis, psoriasis, skin
 CC disorders, AIDS, inflammation, multiple sclerosis, Alzheimer's disease,
 CC Parkinson's disease, asthma, schizophrenia, depression, allergies or
 CC fertility disorders. The nucleic acids may further be used as
 CC hybridisation probes, in chromosome mapping, tissue typing, preventive
 CC medicine, and pharmacogenomics. The present sequence is the amino acid
 CC sequence of the human NOX16 protein of the invention.
 XX
 SQ Sequence 390 AA;

Query Match	83.4%	Score 337;	DB 7;	Length 390;
Best Local Similarity	100.0%	Prod. No. 1.4e-297;		
Matches 337;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 301 CVATHSHSGPQESRAVSISIIEPGEEGPTAGSIVGSGL 338
 Db 301 CVATHSHSGPQESRAVSISIIEPGEEGPTAGSIVGSGL 338
 AC ADE95566;
 XX DT-2004 (First entry)
 DE Human NOX16 protein.
 XX
 XX NOX protein; biochemical stimulation; physiological stimulation;
 KW cardiotonic; antiarrhythmicsclerotic; hypotensive; cytostatic; anorectic;
 KW antirheumatic; antiarthritic; antidiabetic; nephrotropic; dermatological;
 KW immunosuppressive; anti-HIV; antiinflammatory; neuroprotective;
 KW nootropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic;
 KW antidepressant; antiallergic; gynaecological; gene therapy; vaccine;
 KW NOX-associated disorder; cardiomopathy; atherosclerosis; hypertension;
 KW cancer; obesity; rheumatoid arthritis; diabetes; glomerulonephritis;
 KW psoriasis; skin disorder; AIDS; inflammation; multiple sclerosis;
 KW Alzheimer's disease; Parkinson's disease; asthma; schizophrenia;
 KW depression; allergy; fertility disorder; NOX16d.
 XX Homo sapiens.
 XX WO200305245-A2 .
 XX 19-JUN-2003 .
 XX PF 03-DEC-2002; 2002W0-US038594 .
 XX PR 05-DEC-2001; 2001US-033660P .
 PR 07-DEC-2001; 2001US-034885P .
 PR 12-DEC-2001; 2001US-034134P .
 PR 17-DEC-2001; 2001US-034147P .
 PR 17-MAY-2002; 2002US-038081P .
 PR 20-DEC-2001; 2001US-0342592P .
 PR 27-DEC-2001; 2001US-0344297P .
 PR 31-DEC-2001; 2001US-0341903P .
 PR 17-APR-2002; 2002US-037288P .
 PR 15-MAY-2002; 2002US-038081P .
 PR 28-MAY-2002; 2002US-0381495P .
 PR 28-MAY-2002; 2002US-0381334P .
 PR 29-MAY-2002; 2002US-038329P .
 PR 29-MAY-2002; 2002US-0384024P .
 PR 07-AUG-2002; 2002US-0401788P .
 PR 294 HQPQESEKRSVSIIEPGEPTAGSIVGSGLGTAAALGILGGTAAALIGVLMQRQQ 353
 PR 368 RRGEEERKAPENQEEERERAEELNOSEEPEAGESSTGP 404

Db 354 RRGGERKAPENQEEERRAELNQESEPPAGESSTGGP 390

RESULT 14
 ADB95568 ID ADB95568 standard; protein; 390 AA.
 AC ADB95568;
 XX DT 12-FEB-2004 (First entry)
 DE Human NOVX16e protein.
 XX NOVX protein; biochemical stimulation; physiological stimulation; hypotensive; cytostatic; anorectic; cardiotonic; antiartherosclerotic; antiarthritis; antidiabetic; nephrotropic; dermatological; antirheumatic; immunosuppressive; anti-HIV; antiinflammatory; neuroprotective; nocropic; antipsoriatic; antiparkinsonian; antiasthmatic; neuroleptic; antidepressant; antiallergic or gynaecological activities. The DNA sequences of the invention may be useful for gene therapy whilst the protein sequences may allow the development of a vaccine. The protein is useful in the manufacture of a medicament for treating a syndrome associated with a human disease. The invention may be useful in diagnosing, treating or preventing NOVX associated disorders, for example cardiomopathy, atherosclerosis, hypertension, cancer, obesity, skin rheumatoid arthritis; diabetes, glomerulonephritis, psoriasis, Alzheimer's disease, Parkinson's disease, asthma, schizophrenia, depression, allergies or fertility disorders. The nucleic acids may further be used as hybridisation probes. In chromosome mapping, tissue typing, preventive medicine, and pharmacogenomics. The present sequence is the amino acid sequence of the human NOVX16e protein of the invention.

Sequence 390 AA:

Query	Match	Score	Length
OS	83.4‡; Score 337; Pred. No. 1.4e-297; Mismatches 0; Indels 0; Gaps 0;	337	7;
PN	83.4‡; Score 337;保守性 100.0%; Pred. No. 1.4e-297; Mismatches 0; Indels 0; Gaps 0;	337	7;
PN	68 GGGPWDSTARVLPGNSLFLPAGYQDQGIFRQAMMNGKETYSNYRVRVQIOPGKPEBIV 127	68	127
PD	54 GGGPWDSTARVLPGNSLFLPAGYQDQGIFRQAMMNGKETYSNYRVRVQIOPGKPEBIV 113	54	113
PF	128 DSASELTAGVPNKVGTCVSEGSPAGTLSWHDGKPLPVNEKGVSKEQTRRHPETGIFT 187	128	187
XX	114 DSASELTAGVPNKVGTCVSEGSPAGTLSWHDGKPLPVNEKGVSKEQTRRHPETGIFT 173	114	173
PR	05-DEC-2001; 2001US-0336600P. AVAPGGTVLTLCEVPAQSPSPQHMMKDGVPLPLPPSPMLILPEIGPQDGTYSCVATHSS 307	07	307
PR	07-DEC-2001; 2001US-0338288P. AVAPGGTVLTLCEVPAQSPSPQHMMKDGVPLPLPPSPMLILPEIGPQDGTYSCVATHSS 247	12	247
PR	12-DEC-2001; 2001US-0341344P. AVAPGGTVLTLCEVPAQSPSPQHMMKDGVPLPLPPSPMLILPEIGPQDGTYSCVATHSS 293	17	293
PR	17-DEC-2001; 2001US-0341477P. DSASELTAGVPNKVGTCVSEGSPAGTLSWHDGKPLPVNEKGVSKEQTRRHPETGIFT 233	22	233
PR	20-DEC-2001; 2001US-0342594P. DSASELTAGVPNKVGTCVSEGSPAGTLSWHDGKPLPVNEKGVSKEQTRRHPETGIFT 367	27	367
PR	28-MAY-2002; 2002US-0344294P. HGPDQESAVSISIIEPGBEGPAGSVGGGLQTLALGIGGLPAALLGVLRQRQ 353	31	353
PR	29-MAY-2002; 2002US-0344904P. HGPDQESAVSISIIEPGBEGPAGSVGGGLQTLALGIGGLPAALLGVLRQRQ 353	32	353
PR	29-MAY-2002; 2002US-0384024P. HGPDQESAVSISIIEPGBEGPAGSVGGGLQTLALGIGGLPAALLGVLRQRQ 353	33	353
PR	07-AUG-2002; 2002US-0401788P. HGPDQESAVSISIIEPGBEGPAGSVGGGLQTLALGIGGLPAALLGVLRQRQ 353	26	353
PR	26-AUG-2002; 2002US-0406354P. HGPDQESAVSISIIEPGBEGPAGSVGGGLQTLALGIGGLPAALLGVLRQRQ 353	31	353
PR	31-OCT-2002; 2002US-0401788P. HGPDQESAVSISIIEPGBEGPAGSVGGGLQTLALGIGGLPAALLGVLRQRQ 353	32	353
PR	02-DEC-2002; 2002US-00406353. HGPDQESAVSISIIEPGBEGPAGSVGGGLQTLALGIGGLPAALLGVLRQRQ 353	33	353
PA	(CURA-) CURAGEN CORP.	15	390 AA.
XX	Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chilakuru RA;	XX	ADP19670 standard; protein; 390 AA.
PI	Edinger SR, Gerlach VL, Gorman L, Gould-Rothberg BE, Guo Xi;	XX	ADP19670;
PI	Jeffers ME, Ji W, Li L, Malyankar UM, Miller CE, Murphy R;	AC	ADP19670;
PI	Patturajan M, Peyman JA, Rastelli L, Rieger DK, Shenvoy SG;	XX	DT 12-AUG-2004 (First entry)
PI	Smithson G, Starling G, Taupier RJ, Voss EZ, Zhong H, Zhong M;	XX	XX Human LP2007 protein SEQ ID NO:16.
DR	WPI: 2003-513974/48.	XX	XX human; LP2007; antidiabetic; neuroprotective; nootropic;
DR	N-PSDB, ADB95567.	XX	XX antiinflammatory; antirheumatic; cardiovascular; cytotoxic;
XX	New NOVX polypeptides and nucleic acids, useful for preventing or	XX	XX immunosuppressive; nephrotropic; dermatological; gene therapy; diabetes;
PT	treating NOVX-associated disorders, e.g. cancer, cardiomopathy,	XX	XX Alzheimer's disease; inflammation; rheumatoid arthritis; wound;
PT	atherosclerosis or diabetes, and in chromosome mapping, tissue typing or	XX	XX autoimmune disease; multiple sclerosis; cancer; lupus nephritis;
PT	pharmacogenomics.	XX	XX systemic lupus erythematosus.
PS	Claim 2; SEQ ID NO 100; 211pp; English.	OS	XX Homo sapiens.
XX	This invention relates to novel NOVX proteins, and the DNA sequence which	XX	XX Key Peptide
CC	encodes them, having properties related to stimulation of biochemical or	XX	XX Location/Qualifiers
CC		1 . 23	

FT	Protein		/label= signal 24 .390	Qy	128	DSASELTAGVPNPKVGTCVSEGSTPAGTLISWHLDGKPLVPNEKGVSKEQTRRHPEGLT 187
FT			/label= LP2007	Db	114	DSASELTAGVPNPKVGTCVSEGSPAGTLISWHLDGKPLVPNEKGVSKEQTRRHPEGLT 173
XX	WO2004044126-A2.					
XX	27-MAY-2004.					
XX	05-NOV-2003; 2003WO-US0032734.			Qy	188	LQSELMMTPARGGDPRPTFSCSFSPGLPRHRLRTAPIQPRYWEVPLBEVOLVVEPEGG 247
PF	14-NOV-2002; 2002US-0426253P.			Db	174	LQSELMMTPARGGDPRPTFSCSFSPGLPRHRLRTAPIQPRYWEVPLBEVOLVVEPEGG 233
XX	(ELI LILLY & CO ELI.					
PA				Qy	248	AVAPGGTVLTCVPAQSPQTHWMKDQVPLPLPPSPWLLPEIGPDDQGTYSCVATSS 307
XX	P1 Na S, Perkins DR;			Db	234	AVAPGGTVLTCVPAQSPQTHWMKDQVPLPLPPSPWLLPEIGPDDQGTYSCVATSS 293
XX	WPI: 2004-411705/38.			Qy	308	HGPQESRAYSISIIEPGEEGPTAGSVGSSGLGTIALAIGLGGTAALLIGVILWQRQ 367
DR	N-PSDB; ADP19669.			Db	294	HGPQESRAYSISIIEPGEEGPTAGSGSSGLGTIALAIGLGGTAALLIGVILWQRQ 353
XX	New nucleic acid molecules and encoded LP polypeptides (e.g. LP2001 or LP2003) for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, e.g. diabetes or cancer, or for chromosome identification.			Qy	368	RRGGERKAPENQEERERAEELNOSEEEPAGESSSTGGP 404
PT	PT			Db	354	RRGGERKAPENQEERERAEELNOSEEEPAGESSSTGGP 390
PT	PT					
PT	PT					
XX	Disclosure; SEQ ID NO 16; 111pp; English.					
PS						
XX						
CC	The present sequence represents human LP2007, which is used in the exemplification of the present invention. The present invention describes: (1) an isolated nucleic acid (1) comprising DNA having at least 95% sequence identity to a polynucleotide selected from the group consisting of: (a) a polynucleotide having a nucleotide sequence as shown in SEQ ID NO:3, 7, 9, 11 or 13; (b) a polynucleotide encoding a polypeptide or mature form of a polypeptide having the amino acid sequence as shown in SEQ ID NO:4, 8, 10, 12 or 14; (c) a polynucleotide fragment of a polynucleotide as in (a) or (b); and (d) a polynucleotide having a nucleotide sequence which is complementary to the nucleotide sequence of a polynucleotide as in (a), (b) or (c); (2) a vector comprising (1); (3) a host cell comprising the vector; (4) producing an LP polypeptide; (5) an isolated polypeptide produced by the above method and comprising an amino acid sequence comprising about 95% sequence identity to a sequence of amino acid residues comprising LP2001, LP2003, LP2004, LP2005 or LP2006 (SEQ ID NO:4, 8, 10, 12 or 14); (6) a chimeric molecule comprising an LP polypeptide fused to a heterologous amino acid sequence; (7) an antibody which specifically binds to an LP polypeptide described above; (8) a composition (C) comprising a therapeutically amount of an active agent selected from an LP polypeptide, an agonist to an LP polypeptide, an antagonist to an LP polypeptide, an LP polypeptide, an anti-LP polypeptide-encoding mRNA specific ribozyme, and a polynucleotide in combination with a pharmaceutical carrier; and (9) diagnosing or treating a mammal suffering from a disease, condition or disorder associated with aberrant levels of an LP polypeptide. (C) has antidiabetic, neuroprotective, nootropic, antiinflammatory, immunosuppressive, antirheumatic, antiarthritic, pulmonary, cytostatic, nephrotropic and dermatological activities and can be used in gene therapy. The compositions (C) and methods are useful for diagnosing or treating disorders associated with aberrant levels of an LP polypeptide, such as diabetes and its complications. Alzheimer's disease, inflammation, rheumatoid arthritis, wounds, autoimmune disease, multiple sclerosis, cancer, lupus nephritis or systemic lupus erythematosus. They may also be used for chromosome identification. The LP polypeptide can also be used in manufacturing a medicament for the treatment of the above-mentioned diseases, conditions or disorders associated with aberrant levels of the LP polypeptide.					
XX	Sequence 390 AA;					
SQ	Query Match Similarity 83.4%; Score 337; DB 8; Length 390; Best Local Similarity 100.0%; Pred. No. 1.4e-297; Indels 0; Gaps 0;					
Matches 337; Conservative 0; Mismatches 0;						
Qy	68 GGGPWDSVARVLPGNSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYYQIPGKPEIV 127					
Db	54 GGGPWDSVARVLPGNSLFLPAVGIQDEGIFRCQAMNRNGKETKSNYRVRYYQIPGKPEIV 113					

